AY17889 Sorghum b AP002968 Oryza sat AF60203 Sorghum b AF46620 Sorghum b AL606692 Oryza sat AF466199 Sorghum b AK466199 Sorghum b AK106684 Sequence AC120496 Genomic s AP005447 Oryza sat

Zea mays su

AF061282 Sorghum b AC135599 Oryza sat AF46199 Sorghum b AL731588 Oryza sat AP002882 Oryza sat AF061282 Sorghum b

Sequence:

Run on:

Searched:

Database

Result

AF061282 Sorghum b AP002845 Oryza sat AP005840 Oryza sat AP05579 Oryza sat AF61657 Sorghum b AF64051 Oryza sat AL731750 Oryza sat AL732531 Oryza sat AL732531 Oryza sat AL622544 Oryza sat

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131606 CTAAGGTCAGTCTCAATGTGATTTCTTCAGAGTTTTATGGGCATTAAATATGCTGATGTA 131665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD cladd; Panicoideae, Andropogoneae; Sorghum.

1 (bases 1 to 279448)
18lam-Faridi,M.N., Kim,J.-S., Klein,P.E., Stelly,D.M., Price,H.J., Klein,R.R. and Mullet,J.R.

Cytogenetic Analysis of Sorghum Chromosome 3 and Alignment to Rice Chromosome 1 Reveals Expansion of Pericentromeric Heterochromatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L Unpublished (2004)

E 2 (bases 1 to 279448)

S Klein,R.R., Klein,P.E., Mullet,J.E., Minx,P. and Miner,T.L.

Direct Submission

L Submitted (21-JUN-2004) USDA-ARS, Southern Plains Agricultural

Research Center, 2765 F&B Road, College Station, TX 77845, USA

Location/Qualifiers

1. 279448

/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
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/db_xref="taxon:4558"
/map="104.2-11.2 CM"
/clone="BAC 88M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 279448;
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                                                                                                                                                                                                AF061282
AC135599
AF466199
OSJN00241
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AC120496
AP005447
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AP002845
AP005420
AP005579
                                AY177889
AP002968
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AY661657
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Sorghum bicolor
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Matches 162; Conserv
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                                                                                                        Query Match
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SOURCE
ORGANISM
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AY661656
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AY14442 Sorghum b
L2175 Saccharum h
AR412080 Sequence
AR44313 Sequence
AR43375 Sequence
AR43375 Sequence
AR43379 Sequence
AR43379 Sequence
AR43379 Sequence
AR43379 Sequence
AR41317 Sorghum b
AF114171 Sorghum b
AF14471 Sorghum b
AF14471 Sorghum b
AF14471 Sorghum b
AF14471 Sorghum b
AF146200 Sorghum b
AF046200 Sorghum b
                                                                                                                     February 15, 2005, 15:29:19 ; Search time 12873 Seconds (without alignments) 11352.515 Million cell updates/sec
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                                                                                                                                                                                                                                       1 tctagagcataggcattgta......gggctatgtcaagtccatgg 3016
               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                 4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                                                                                                                                                  Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                      - nucleic search, using sw model
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AR488131
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AF114171
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AY542311
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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PLN 03-JUL-2004

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QLOSLSLIDVPNITAKCISOFRVOKKLSVSSFVLLNOMLKAEGFIVPPNLGLHVCKEP
SASFGECANLLSVKHLDIMDCKMESLPGNLKFLSSLESLDIGICPNITSLPVLPSSLQ
RITIYGCDDLKKNCREPDGESWPQISHIRWKHFYE"
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CFLYCSLFPKGHKYKPDELVHLWVABGLVGSCNLSSMTIEDVGRDYRFBELSGSFFQL
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LTKLSIETCPLLMFVSKNELDQHDLRENIMKTEDLASKLASMWEVNSGSNIREVLAED
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LTKLDLLAVRGCWCLRSLGGSHAAPSLSRLYCIDCPSLDLAGAAESMSFNLAGDLYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQFDLVIQAAEKSPHKGKLEAWLRRLKEAFYDAEDLLDEHEYNLLKRKAKSGKDPLLG
EDETSSIASTIMKPFHTAKSKARNLLPENRRLISKMNEIKAILTEAKELRDLLSIAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'translation="MADLALAGLRWAASPIFNKLLNEASAYLSVDMVRELQKLEATVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTTGLGWPAVPATIVPPTTVTSLSTSKVFGRDKDRDRILDFLLGKTAADEASSTRYSS
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PCI DNLDTLQCKLRDILQKSQKFLLVLDDDWFEKSDSETEWFQLLDPFVSKQMGSKVL
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/note="rph1-3; truncated at 5' end; rust resistance gene;
                                                                                                             . >18428))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(joīn(<19109. .19204,19331. .>19486))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
complement(join(19109. .19204,19331. .19486))
/gene="lB"
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NTACEGWPVVPATIVPPTTVTYFPHQRFSVVTRIVII"
complement (<17525. .>18428)
                                                                                                                .17710,18303.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="putative Rp1-like protein"
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/evidence=not_experimental
<20054. .>23947
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/codon_start=1
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/gene="rph1-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /qene="rph1-2
                                                                                                                                           gene="1A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene≃"1B'
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                                                           131666 ACATCGTATTAATAAAGTGAGAGATGATAAGAGTTTCATGGGGAGCGAGAGAGTTTCATC 131725
                                                                                                                                                                                             131726 CCCATAAAACTCTTCTGCACTGTTTCTAAATCAGATGTGTTGGAAACTGGGACACGAAA 131785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQFDLVIQAAEKSAYRGKLEAWLRRLKEAFYDAEDLLDEHEYNLLKRKAKŠGKDPLVG
EDETSSIASTILKPLRAAKSRAHNLLPENRKLISKMNELKAILKEANELRDLLSIPPG
                       1517 ACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGATTCATG 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLN 08-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
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Ramakarishna, W., Emberton, J., SanMiguel, P., Ogden, M., Llaca, V., Messing, J. and Bennerzen, J.L.

Comparative sequence analysis of the sorghum rph region and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-AUG-2002) Biological Sciences, Purdue University,
Hansen Bldg, West Lafayette, IN 47907, USA
Location/Qualifiers
                                                                                                                                        1577 GGGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTGGTAAGAGGCCCATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 268433)
Ramakzishna, W., Emberton, J., SanMiguel, P., Ogden, M., Llaca, V.,
Linton, E., Messing, J. and Bennetzen, J.L.
Sequence and physical map analysis of Rpl region of maize and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 268433)
Ramakrishna, W., Emberton, J., SanMiguel, P., Ogden, M., Llaca, V.,
Linton, E., Messing, J. and Bennetzen, J.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                     AY14442 268433 bp DNA linear PLN 08-JAN
Sorghum bicolor BAC 95A23/98N8.1 Rph region, partial sequence.
AY144442
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<11707. .>12300
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'codon_start=1
evidence=not_experimental
product="truncated Rph1-1 protein"
'protein_id="AAO16684.1"
'db_xref="GI:27542751"
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Plant Physiol. 130 (4), 1728-1738 (2002)
22369073
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/evidence=not experimental
-211707. .-1230
/gene="rph1-1"
                                                                                                                                                                                                                                                         1637 ATCTCTAGTGACACTGACCTAAGATGAGAT 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .268433
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="BAC 95A23/98N8.1"
complement(1600..6611)
/note="contains LTRs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorghum bicolor (sorghum)
Sorghum bicolor
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'gene="rph1-1"
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238423
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                                                                                          238483
                                               1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharum hybrid cultivar H65-7052
Saccharum hybrid cultivar H65-7052
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NILEPRNRPQLVMAVCMPAFQILTGINSILFYAPVLFQSMGFGGNASLYSSVLTGAVL
SSTILSIGTVDRLGRRKLISGGTQM)VCQVIVAVILGAFRGADKQLSSRSYSTAVVV
VICLFVLAFGWSWGPLGGWTVPDSEIFPLETRSAGQSITVANVLLFTPALAQAFLSLLCA
FKFGIFLFFAGWITVMTVFVCVFLPETKGVPIEBNVLLMRKHWFWKKVMPADMPLEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLN 02-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'translation="IERGRVEEGRRVLERIRGTADVDAEFTDMVEASELANTIEHPFR
                                                                                                                                    1513 TGTGACACCGTATTGATGAAGAGAGAGATAAGAGTTTCATGCGAGTAGAGAGGTTT
                                                                                                                                                                                 238482 TGTGGCACTATATTAATGAAGAGAGATGGTAAGAGTTTCATGGGAGTAGAGAGTTT
                                               GTTTCTAAGGCCAGTCTCAGTGGGGTTTTCATCAGAGTTTCATGGACATTAAATAAGCTGA
                                                                                       238542 GCTTCTTAGGCCAGTCTCAATGAGGCTTTCATTAGAGTTTCATGACATTAAATATGCTGA
                                                                                                                                                                                                                              CATGGGGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTGGTAAGAGGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Divect Submission
Direct Submission
Submitted (14-JUL-1993) Robert Bugos, Hawaiian Sugar Planters'
Association, Experiment Station, Alea, HI 96701-1057, USA
Location/Qualifiers
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1215 bp mRNA linear PLN 02-P
hybrid cultivar H65-7052 glucose transporter mRNA,
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    1215
/organism="Saccharum hybrid cultivar H65-7052"

52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1215)
Blugos,R.C. and Thom,M.
Glucose transporter CDNAs from sugarcane
Plant Physiol. 103 (4), 1469-1470 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=3
/product=rglucose transporter"
/protein_id="AAA\8533.1"
/db_xref="G1:347853"
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                 238362 richárachtranggariggcerra 238337
                                                                                                                                                                                                                                                                                                                      TGAAATCTCTAGTGACACTGACCTAA 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:50503"
/tissue_type="leaf"
<1. .866
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="H65-7052"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="putative"
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Best Local Similarity 82.4%;
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 1215)
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  Matches 154; Conservative
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partial cds.
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                                                                                       complement(join(<27459. .27638,27696. .27866,28135. .>28260))
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                                                                                                                                                            .28260))
                                                                                                                                                                                                                                                                                                                                         /trānslation="MEGSAFGRLVRCRRWNTTQENGRTADGEMLNRTGTDIAVLDWGY
KIIAHRPQLNLMAMITSRLQRDSQASTRSRPSTHGLHLPKRDRQDSIPATVPGGESFG
GCGGRRQTPARGGSGGGGVTATRPAAEEGETDTLVGLVGCSCEVSEELLLTLVES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/product="truncated rpl-4 protein"
/protein_id="AAO16687.1"
/db_xref="G1:2754754"
/translation="MAD1AAGLRWAASPIFNKLLNBASAYLSVDMYRELQKLBATVL
PQFDLVIQAAEKSPHKGKLEAWLRRLKEAFYDAEDLLDEHEYNLLKRKAKSGKDPLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDETSSIASTIMKPFHTAKSKARNLLPENRRLISKMNBIKAILTEAKELRDLLSIAPG
NTTGLGWPNVPATIVPPTTVTSLSTSKVFGRDKDRDRIVDFLLGKTAADEASSTRYSS
LAIIGAGGMGKSTLVQYVYNDKRIEEGFDIRMCVGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MKLHQVKKIKGAGSRVAGASVDNEHEVAEVVDGTLEQALHFKRT
NRQPAKNKSHGEDTDGAAGLLLLAGKRKKQGNWKVEKEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by retrotransposon insertion; similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16834. .37160
'note="rph1-5; truncated rust resistance gene; similar to
                                                                                                                                    /product="hypothetical protein"
complement(join(27459. .27638,27696. .27866,28135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .42816,42947.
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/note="similar to Arabidopsis thaliana RPT2 gene"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
complement(join(<28943. .29038,29166. .>29321))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
complement(join(28943. .29038,29166. .29321))
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complement (join(40727. .42601,42717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transposon="Kaema-1 retrotransposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="truncated rp1-4 protein"
                                                                                                                                                                                                                       /codon_start=1
/evidence=not experimental
/evidence=not experimental
/product="hypothetical protein"
/protein_id="AAO16707.1"
/db_xref="G1:27542774"
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evidence=not experimental
product="hypothetical protein"
protein_id="AAO16708.1"
db_xref="GI:27542775"
                                                                                                                                                                                                  note="similar to EST BE362870"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="rust resistance gene"
/evidence=not_experimental
<29889. .>30653
/gene="rhp1-4"
                       complement (<27459. .>28260)
                                                                                                                                                                                                                                                                                                                                                                                                              complement (<28943. .>29321)
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                                                                    'evidence=not experimental
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/note="contains LTRs"
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/gene="rhp1-4"
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Gaps

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Indels

4.1%; Score 122.8; DB 8; Length 268433; 74.8%; Pred. No. 1.2e-20;

Query Match Best Local Similarity

1510

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PAT 18-DEC-2003
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                                                                                                                        1855 GAIGIGGCACCGIAITGAIGAAGAGAGAGATGAIAAGAGIIICAIGGAAITAGAGAGAI 1796
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                                                                                   Gaps
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Unclassified.
Unclassified.
1 (bases 1 to 3688)
Albert, H.H. and Wei, H.
Sugarcane UB19 gene promoter and methods of use thereof Patent: US 6706948-A 10 16-MAR-2004;
Location/Qualifiers
e /oraganism="unknown"
/mol_type="genomic DNA"
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                                                         Score 118.6; DB 6; Length 3688; Pred. No. 1.1e-19;
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3.9%; Score 118.6; I
Best Local Similarity 86.0%; Pred. No. 1.1e
Matches 166; Conservative 0; Mismatches
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Sequence 10 from patent US 6706948.
AR488131 GI:47253896
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Sequence 3 from patent US 6638766.
AR412075 GI:40164628
         /organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 86.0
Matches 166; Conservative
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AR488131/c
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             968 GCCAGTCTCACTGGGGTTTCATTAGAGTTTTATGGGCATTAAATGTGCTGATGTGGGCATC 1027
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Albert, H.H. and Wei, H.
Sugarcane ubig gene promoter sequence and methods of use thereof
Patent: US 6686513-A 10 03-FBB-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGGACTTTCATGGACATTAAATAAGCT
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GCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATGTGACACC
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Best Local Similarity 86.0%; Pred. No. 1.1e-19;
Matches 166; Conservative 0; Mismatches 24; Indels 3;
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1 (bases 1 to 3688)
Albert,H.H. and Wei,H.
Promoter of the sugarcane UBI4 gene
Patent: US 6638766-A 10 28-OCT-2003;
Location/Qualifiers
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US 6638766.
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Sequence 10 from patent
AR412080
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AR412080/c
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Albert,H.H. and Wei,H.
Sugarcane UBI9 gene promoter and methods of use thereof
Patent: US 6706948-A 3 16-MAR-2004;
Location/Qualifiers
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llarity 86.0%; Pred. No. 1.1e-19;
Conservative 0; Mismatches 24
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Albert,H.H. and Wei,H.
Promoter of the sugarcane UB14 gene
Patent: US 6638766-A 8 28-OCT-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 from patent US 6638766. AR412079 GI:40164632
                                                                               3691 bp
Sequence 3 from patent US 6706948.
AR488126
AR488126.1 GI:47253891
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/organism="unknown"
/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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 1735 GCCATAAAATCCC 1723
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AR412079/c
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AR488126/c
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Albert,H.H. and Wei,H.
Sugarcane ubi9 gene promoter sequence and methods of use thereof
Patent: US 6686513-A 3 03-FEB-2004;
Location/Qualifiers
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                                                                                                                                                                                                                           Score 118.6; DB 6; Length 3691;
Pred. No. 1.1e-19;
0; Mismatches 24; Indels 3;
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86.0%; Pred. No. 1.1e-19;
ive 0; Mismatches 24; Indels
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                                                           1 (bases 1 to 3691)
Albert, H. H. and Wei, H.
Promoter of the sugarcane UB14 gene
Patent: US 6638766-A 3 28-OCT-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3691 bp
Sequence 3 from patent US 6686513.
AR473375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
                                                                                                                                               1. .3691
/organism="unknown"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                           3.9%;
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Best Local Similarity 86.09
Matches 166; Conservative
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                                           Jnclassified.
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Unclassified.
                                                                                                                                                                                                                                              Similarity
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AR473375/c
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Query Match 3.9%;
Best Local Similarity 86.0%;
Matches 166; Conservative
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  1795 TTTACGAAGATGAAACTCTTCCTGCACTGTTTTCCAAATATGGGTTGCATTAATAACATG 1736
                                      1571 TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
                                                                                                                                                                      PAT 20-FEB-2004
                                                                                                                                                                                                                                                                   1 (bases 1 to 5174)
Albort, H.H. and Wei, H.
Sugarcane ubi9 gene promoter sequence and methods of use thereof
Patent: US 6686513-A 8 03-FEB-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT
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Unknown.
Unclassified.
Unclassified.
I (bases 1 to 5174)
Albert,H.H. and Wei,H.
Sugarcane UB19 gene promoter and methods of use thereof
Patent: US 6706948-A 8 16-MAR-2004;
Location/Qualifiers
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Best Local Similarity 86.0%; Pred. No. 1.1e-19;
Matches 166; Conservative 0; Mismatches 24; Indels 3;
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Sequence 8 from patent US 6706948.
AR488130
                                                                                                                                                                      AR473379 5174 bp
Sequence 8 from patent US 6686513.
AR473379 GI:42708830
                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
/mol_type="genomic DNA"
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AR473379/c
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Saccharum hybrid cultivar H32-8560
Saccharum hybrid cultivar H32-8560
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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/cultivar="H13-8560"
/db xref="taxon:50502"
/note="interspecific hybrid; lineage includes Saccharum officinarum and Saccharum spontaneum"
/note:"MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG
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Isolation and transfent expression of two promoters from Isolation and transfent expression of two promoters from Unpublished
2 (bases 1 to 5174)
Wei, H., Albert, H.H. and Moore, P.H.
Birect Submission
Su
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transposable element"
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Length 5174;
                                                                                                    24; Indels
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/codon start=1
/product="polyubiquitin"
/protein id="AAG67552.1"
/db_xref="G1:3789942"
     Score 118.6; DB 6;
Pred. No. 1.1e-19;
0; Mismatches 24;
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join(2249. .2313,3689. .5079)
gene="ubi9"
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2249. .2313
/gene="ubi9"
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/gene="ubi9"
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AF093505
AF093505.1 GI:3789941
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/gene="ubi9"
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PAGKOLEBGRTLADYNIOKESTILALVIRIRGGMOI FVKTLIGKTITLEVESSDTIDNV KAKLODKEGI PPDQQRX I FAGKQLEDGRTLADYNIQKESTLHLVIRLRGGMOI FVKTL TGKTILLEVESSDTIDNYKAKLODKEGI PPDQQRST I FAKTLOKEGI PPDQQRST I HAVYKAKLODKEGI PROGRESTILAYNIQKEST I LALVIRLRGGMOI FVKTLIGKTLIDRKRI DPDQQRST QLEDGRTLAXYNIQKESTLHLVIRLRGGMOI FVKTLIGKTITLEVESSDTIDNYKAKI QDKKGI PPDQQRXI FAGK QDKKGI PPDQQRX I FAGK QLEDGRTLADYNIQKESTLHLVIRLRGGQ"
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Unpublished
Unpublished
Liaca, V., Lou, A., Young, S. and Messing, J.
Liaca, V., Lou, A., Young, S. and Messing, J.
Liaca, Submission
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translation="MQIPVKTLTGKTITLEVESSDTIDNVKAKIQDKEGIPPDQQRLI
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1 (bases 1 to 18399)
Llaca,V., Lou,A., Young,S. and Messing,J.
Retrotransposable elements of Sorghum bicolor
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/clone="BAC 25.M18"
/clone=lib="Woo et. al., Nucl. Acids Res. 22:4922-4931,"
3517. 3644
/rpt_type=dispersed
/rpt_family="HCSR-1"
/rpt_family="HGSR-1"
/rpt_family="1556,4699. >5541)
/product="putative beta-ketoacyl-CoA synthase"
join(3841. 4596,4699. 5541)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGGGTTTCATGGACATTAAATAAGCT
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/note="similar to Oryza sativa EST clones E10604_1A,
/codon_start=1
/product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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/protein_id="AAD27560.1"
/db_xref="GI:4680197"
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Sorghum bicolor BAC clone 25.M18, complete sequence.
AF114171
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/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
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                                                                                                                                                                                                                                                                       4835. .5079
/gene="ubi9"
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LLDLACYKPGAEHAVTRETEWRLVVGYGTFSDDSLAFORKILERSGLGGGTYLERALT
SASPUPPCWAEARREAEAVWEGAVDOLLAKTGVRAGDIGIVVNSGLFSPTSLGAMIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEVHREARRQERAQDGGGDAERHEDDEEVVVVAFETHVRRGVEVEEHQLRRERRRYG
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PESSSSRSGEEEVVVRTGFHARTRNVDGDAACRDAEHQTRHRPTSRNSVPGSTWPLND
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complement(19738. 19888)
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                           IDRATSFITTFTVY I ERLIGMEIHCKDVODOBIRSILIRPOPDARVÄNFKI DEVYPSR
DNAVRLSDDNIQTNI ESPSPVFLVQI APRDPPPLSPVCSRNLCRPGAHVACALCVWRG
RCRCRRRWDNTTGRQML I FMPADYYTHVITVI I YDDDDSI I HALLLVLLACGOLLALC
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Llaca, V., Lou, A., Young, S. and Messing, J.

Retrotransposable elements of Sorghum bicolor
Unpublished

2 (bases 1 to 183990)

Llaca, V., Lou, A., Young, S. and Messing, J.

Direct Submission

Submitted (15-DEC-1998) Waksman Institute, Rutgers University, 190

Frelinghuysen Rd., Piscataway, NJ 08854-8020, USA
SLDLLNISETFAFVASLLHPESRAAALATARSSCSLAAASGSTAQSASSTLKRWPSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161714 ACTAAATATGCTGATGTGACACTATATTAATGAAGAGAGGGGGTGATAAGAGTTTCATAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 106.4; DB 8; Length 183990;
Pred. No. 2.6e-16;
0; Mismatches 41; Indels 2; 0
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Sorghum bicolor BAC clone 25.M18, complete sequence.
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Best Local Similarity 76.9%;
Matches 143; Conservative 0
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RAVKHGSTGSTPAAERSPPFRWYKNTCLKI ENAARRI STSVEVSSAPTINQI PSITA
RAVKHGSTGSTPAARTAAAANPEFRRFFTSLETNNGARLDLLQREHEKKNKK
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DGTDEGESDESMNI I RDR I VDALTKEKTRARRABGSLINTRGGGGGRSVPQAVRSHGAL
RRPPLVVSGGGGRRRRRDGAVQSSHVQPR I CTAHHLQOEPRLVQGGGIQQVAVHQVRA
ARRREGRRRRPTRAFTARARRARRARRARRA
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product="hypothetical protein".
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LRIELAQKNKKOKTTKESTPSNVEASNNDEI PEVAAPDSEERKRPKGGKQVKQARDD
ASLAVLEKMLEKKEARELERDKAREASLEI ERASLEI EKAALEI EKKRLSNEEKKIEA
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n complement (5285 . 5905)

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/ Tpt_family
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/rpt_form="Miles of the family of the
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Search completed: February 16, 2005, 07:44:40 Job time : 12881 secs

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RESULT 1
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Add 66210 Sugarcane
Add 40707 Plant cDN
Abk 93956 cDNA enco
Add 86070 Corn seed
Ada 72001 Rice gene
Adc 08563 Rice DNA
Add 1371 Plant cDN
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Aaz99112 Phosphoen
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Ada72420 Rice gene
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Aaz28433 Ubi9 gene
Adk66205 Sugarcane
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11518.671 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                             4390206 segs, 2959870667 residues
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Listing first 45 summaries
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ALIGNMENTS

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New isolated nucleic acid comprises an o-methyl transferase (OMT) promoter and an exogenous nucleic acid, useful as a promoter for altering carbon metabolism in a plant cell or for driving expression of insecticidal proteins in sugarcane.
                                                                                                                                                                     O-methyl transferase; OMT; promoter; stem-specific; defence-inducible; carbon metabolism; insecticidal; pest tolerance; plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emani C;
                                                                                                                              Sugarcane O-methyl transferase (OMT) promoter DNA SegID 1.
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261. .2664
261. .2664
2849. .2855
/*tag= b
3013. .3015
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/note= "Start codon (AUG) of OMT"
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ВЪ.
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ADR21935 standard; DNA; 3016
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                                                                                   (first entry)
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Kumpatla SP;
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This invention relates to a novel nucleic acid molecule that comprises an O-methyl transferase (OMT) promoter and an exogenous nucleic acid.

Specifically, it refers to a stem-specific promoter active in plants that exhibits enhanced specificity in regulating gene expression in stem tissues and in response to induction by external stimuli such as plant deference-inducing agents. The present invention describes a bacterial cell comprising an expression vector that can be used to transform a monocot plant such as sugarcane, sorghum, rice, maize or hybrids thereof, in order to upregulate localised expression. In particular, this nucleic acid is useful as a promoter for altering carbon metabolism in the sucrose accumulating tissues, and for driving expression of insecticidal gevelopment of improved peets and disease tolerant rice plants. This polynucleotide sequence is the OMT promoter DNA sequence of the SEQ ID NO 1; 56pp; English

Seguence 3016 BP; 870 A; 587 C; 698 G; 861 T; 0 U; 0 Other;

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} &	1141	ATAAAAGCTATCATGTCGACCGGCACGTTTAATATTTAACTTATACCATATG 1
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λo	1261	AGCATGAAGCTCTGAACTATGAATTTATGATGTATTGTGGC 132
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ò	1381	CATTTGG 144
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λo	1441	TCAGTGGGGTTTCATCAGAGTTTCATGGACAT 15
qq	1441	CATCAGAGTTTCATGGACAT 150
ò	1501	TGATAAGAGTTTCATGCGAG 156
οp	1501	TGATGTGACACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAG 156
ò	1561	HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI
ΩÞ	1561	162
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                                                                           2941 AGCACTGATCAGCAGGCCGTGCTGGATGCTCAGCTCCAGCTCTGGCACCACCCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1914 AGTITITCIGAGGCCCGICTCAGT-GGATTICATCAGAGTITCATGGACATTAAATAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleotide sequences derived from sugarcane polyubiquitin genes useful in regulating expression of nucleic acid sequences in monocotyledonous and dicotyledonous plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ubi4 and ubi9) are used to create plants with commercially useful phenotypes. High levels of protein expression aid the generation of plants which exhibit commercially important phenotypic properties su
                                                                                                                                                                                                                                                                                                                                                                                                                           Sugar cane ubi9 gene fragment used in the construction of pubi9-GUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pest and disease resistance, resistance to environmental stress and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ubiquitin gene; ubi9; promoter; initiation codon; intron; monocoty dicotyledon; disease resistance; environmental stress; sugar cane; pubi4-GUS; reporter plasmid; beta-glucuronidase; GUS; ss.
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Pred. No. 5.4e-22;
0; Mismatches 24; Indels
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(USDA ) US DEPT OF AGRICULTURE.
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CGCCCTGGAGGGATTAGATACAACTTCAATTATATCTTAGGGCCCCTCCAATATTGTCAG 1980
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                                                                                                                                                                                                                                                                                                                                                                                                                         2821 GAATTCGGAAGTACTATAAACGGGAGCCTATAAATGGAGACGTTTTGCATCATGAGGCTA 2880
                                                                                                                                                                                                                                                                     AGTCAAGGTTGTGCCTAACAAACTGGGGTTCACATGTAAAACACGTTCATGCCTTAGAAA
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                                                                                                                                                       CGGCCTGGAGGGATTAGATACAACTTCAATTATATCTTAGGGCCCCTCCAATATTGTCAG
                                                                                                                                                                                                                                              2161 CTAAGAGCCCAACACCTGACTGTACTGTTGAAGGTGTCCTAGTTGGAGTGGTCGATCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides nucleic acids having promoter activity. The invention is directed to isolating nucleic acid sequences from sugarcane polyubiquitin genes which are capable of directing constitutive expression of a nucleic acid of interest in monocotyledonous and dicotyledonous plants. The invention is useful in generating transgenic plants which exhibit commercially important phenotypic properties. The present sequence is sugarcane polyubiquitin ubi9 gene promoter DNA.
          GATGTGACACCGTATTGATGAAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGGT 1570
                                                                         1795 FITACGAAGATGAAACTCTTCCTGCACTGTTTTCCAAATATGGGTTGCATTAATAACATG 1736
                                                           TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic plant cell comprising the sugarcane ubi9 polyubiquitin gene promoter, useful for generating transgenic plants exhibiting important phenotypic properties, such as pest, disease and environmental
                                                                                                                                                                                                                                                                                             Polyubiquitin; monocotyledonous; dicotyledonous; transgenic plant; phenotypic; sugarcane; plant; ds.
                                                                                                                                                                                                                                                                        Sugarcane polyubiquitin ubi9 gene promoter DNA.
                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "Upstream of 5' UTR"
2249. .2313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 10; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                   BP
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99US-00270976.
                                                                                                                                                                                                  ADK66212 standard; DNA; 3688
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                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= .b
2314. .3688
/*tag= c
                                                                                                              GCCATGAAATCTC 1641
                                                                                                                                      sccaradarccc 1723
                                                                                                                                                                                                                                                  (first entry)
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(UYHA-) UNIV HAWAII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albert HH, Wei H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stress resistance.
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17-MAR-1999;
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                1511
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                                                                                                                                                                                                                            ADK66212;
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ADK66212/
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3.9%; Score 118.6; DB 12; Length 3688; 86.0%; Pred. No. 5.4e-22;

Best Local Similarity

Query Match

Sequence 3688 BP; 844 A; 862 C; 925 G; 1055 T; 0 U; 2 Other;

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This sequence contains the sugar cane ubiquitin gene ubi9 initiation codon, and the upstream sequence of the gene including the 5, untranslated region. The gene has an intron immediately upstream of the intiation codon. The ubi9 gene is used in the invention as it has linked promoter activity, and the polyubiquitin genes are useful in regulating high expression of nucleic acid sequences in monocotyledonous and dicotyledonous plants. The nucleic acid sequences (ubi4 and ubi9) are used to create plants with commercially useful phenotypes. High levels of protein expression aid the generation of plants which exhibit commercially important phenotypic properties such as peet and disease resistance, resistance to environmental stress and improved qualities
                                                                                                                                                           1795 TTTACGAAGATGAAACTCTTCCTGCACTGTTTTCCAAATATGGCTTGCATTAATAACATG 1736
                                                                                                                                           TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ubiquitin gene; ubi9; promoter; initiation codon; intron; monocotyledon; dicotyledon; disease resistance; environmental stress; sugar cane; ss.
1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT
                                                                     1511 GATGTGACACCGTATTGATGAAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGT
                                                                                           1914 AGTTTTCTGAGGCCCGTCTCAGT-GGATTTCATCAGAGTTTCATGGACATTAAATAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleotide sequences derived from sugarcane polyubiquitin genes useful in regulating expression of nucleic acid sequences in monocotyledonous and dicotyledonous plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ubi9 gene fragment including initiation codon and upstream sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
2201. .2208
/*tag= a
2249. .2313
/*tag= b
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                                                                                                                                                                                                                                                                                                                                        AAZ28433 standard; DNA; 3691 BP.
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(USDA ) US DEPT OF AGRICULTURE.
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99US-00270976.
                                                                                                                                                                                                                                                  1735 GCCATAAATCCC 1723
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New nucleotide sequences derived from sugarcane polyubiquitin genes
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3689. .3691
                                                                                                                                                                                                                                                                                                                                              Sugar cane ubiquitin 9 (ubi9) gene.
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(USDA ) US DEPT OF AGRICULTURE.
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                                                                         1914 AGTTTTCTGAGGCCCGTCTCAGT-GGATTTCATCAGAGTTTCATGGACATTAAATAAATAGGCT 1856
                                                                                                          TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transgenic plant cell comprising the sugarcane ubi9 polyubiquitin gene promoter, useful for generating transgenic plants exhibiting important phenotypic properties, such as pest, disease and environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides nucleic acids having promoter activity. The invention is directed to isolating nucleic acid sequences from
                                                                                                 1511 GATGTGACACCGTATTGATGAAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGT
                                                            1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT
                                            Gaps
                                                                                                                                                                                                                                                                                                                  Polyubiquitin; monocotyledonous; dicotyledonous; transgenic plant; phenotypic; sugarcane; plant; ds.
                                          3,
                          Length 3691;
       Sequence 3691 BP; 845 A; 862 C; 927 G; 1055 T; 0 U; 2 Other;
                                           24; Indels
                       DB 2;
                        Query Match 3.9%; Score 118.6; DB 2
Best Local Similarity 86.0%; Pred. No. 5.4e-22;
Matches 166; Conservative 0; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                           of 5' UTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 3; 79pp; English.
                                                                                                                                                                                                                                                                                                 Sugarcane polyubiquitin ubi9 gene #1.
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/note= "Upstream
2249. .2313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1795 TTTACGAAGATGAAACTCTTCCTGCACTGTTTTCCAAATAAGGGTTGCATTAATAACATG 1736
sugarcane polyubiquitin genes which are capable of directing constitutive expression of a nucleic acid of interest in monocotyledonous and dicotyledonous plants. The invention is useful in generating transgenic plants which exhibit commercially important phenotypic properties. The present sequence is sugarcane polyubiquitin ubi9 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ubiquitin gene; ubi4; promoter; initiation codon; intron; monocotyledon; dicotyledon; disease resistance; environmental stress; sugar cane; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1511 GATGTGACACCGTATTGATGAAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGTGGCACCGTATTGATGAAGAGAGAGATGATAAAGAGAGTTTCATGGAATTAGAGAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1914 AGTTTTCTGAGGCCCGTCTCAGT-GGATTTCATCAGAGTTTCATGACATTAAATAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1571 TICATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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ش
                                                                                                                                                                                                                                                                                                                    DB 12; Length 3691;
                                                                                                                                                                                                                                           Sequence 3691 BP; 845 A; 862 C; 927 G; 1055 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "ubig"

/note= "Ubiquitin 9 protein"

/ransl_except= (Pos:4043. .4045, aa.Xaa)

/transl_except= (Pos:4316. .4318, aa.Xaa)

/transl_except= (Pos:4499. .4501, aa.Xaa)

/transl_except= (Pos:4499. .4501, aa.Xaa)

/note= " Xaa = Uhknown"
                                                                                                                                                                                                                                                                                                                    3.9%; Score 118.6; DB 12; Length
86.0%; Pred. No. 5.4e-22;
tive 0; Mismatches 24; Indels
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protein"

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1511 GATGTGACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGAT 1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1571 TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1795 irracsaasaitsaakereireersekeritrireeaaatareserrsearraaaakaears
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides nucleic acids having promoter activity. The invention is directed to isolating nucleic acid sequences from sugarcane polyubiquitin genes which are capable of directing constitutive expression of a nucleic acid of interest in monocotyledonous and dicotyledonous plants. The invention is useful in generating transgenic plants which exhibit commercially important phenotypic properties. The present sequence is sugarcane polyubiquitin ubi9 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transgenic plant cell comprising the sugarcane ubi9 polyubiquitin gene promoter, useful for generating transgenic plants exhibiting important phenotypic properties, such as pest, disease and environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1451 AGGITICTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5174 BP; 1178 A; 1270 C; 1313 G; 1398 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 5174;
                                                     / transl excepte (pos:3818 .3820, aa:Ile) / transl excepte (pos:4274 .4276, aa:Ile) / transl excepte (pos:4289 .4291, aa:Gln) / transl excepte (pos:4281 .4331, aa:Gln) / transl excepte (pos:4607 .4609, aa:Ile) / transl excepte (pos:4607 .4609, aa:Ile) / note= "Xaa may be any amino acid" / note= "Xaa may be any amino acid" / transl excepte (pos:4499 .4501, aa:Xaa) / note= "Xaa may be any amino acid" / transl excepte (pos:4499 .4501, aa:Xaa) / note= "Xaa may be any amino acid" / note= "Xaa may be any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.9%; Score 118.6; DB 12; Length
86.0%; Pred. No. 6.5e-22;
tive 0; Mismatches 24; Indels
                                           polyubiquitin ubi9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 8; 79pp; English.
                                             product= "Sugarcane
້ວ
   note= "Fragment
                                                                                                                                                                                                                                                                                                                                                                   98US-0078767P.
99US-00270976.
                                                                                                                                                                                                                                                                                                                                      20-OCT-2000; 2000US-00693467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1629 GCCATGAAATCTC 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1735 GCCATAAATCCC 1723
                   .4834
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Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (USDA ) US SEC OF AGRIC.
(UYHA-) UNIV HAWAII.
                                 *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-106365/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albert HH, Wei H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ADK66211.
GENBANK; AF093505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stress resistance
                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1998;
17-MAR-1999;
                                                                                                                                                                                                                                                                             US6686513-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TICATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is sugar cane polyubiquitin ubi9 gene. The invention relates to nuclectide sequences derived from sugar cane polyubiquitin genes. The ubi4 and ubi9 genes are used in the invention as they have linked promoter activity, and the polyubiquitin genes are useful in regulating high expression of nucleic acid sequences in monocotyledonous and dicotyledonous plants. The nucleic acid sequences (ubi4 and ubi9) are used to create plants with commercially useful phenotypes. High levels of protein expression aid the generation of plants which exhibit commercially important phenotypic properties such as pest and disease resistance, resistance to environmental stress and improved qualities
                                                                                                                                                                                                                                                                                                                                                            1914 AGTTTTCTGAGGCCCGTCTCAGT-GGATTTCATCAGAGTTTCATGGACATTAAATAAGCCT
                                                                                                                                                                                                                                                                                                                                           1451 AGGITICIAAGGCCAGIGICAGAGGGGTITCATCAGAGTTICATGGACATTAAATAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                        1511 GATGTGACACCGTATTGATGAAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polyubiquitin; monocotyledonous; dicotyledonous; transgenic plant; phenotypic; sugarcane; plant; gene; ds.
                                                                                                                                                                                                                                                   Sequence 5174 BP; 1178 A; 1270 C; 1313 G; 1398 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                               Score 118.6; DB 2; Length 5174; Pred. No. 6.5e-22; 0; Mismatches 24; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= c
note= "Bases used in reporter constructs"
        useful in regulating expression of nucleic acid sequences monocotyledonous and dicotyledonous plants.
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/note= "Upstream region"
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/*tag= d
2314. 3688
/*tag= 6
3602. 3612
/*tag= f
// note= "Fragment B"
/*tag= 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .3688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= b
note= "Fragment A"
...2248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugarcane polyubiquitin ubi9 DNA.
                                                      Example 1; Fig 8; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK66210 standard; DNA; 5174 BP
                                                                                                                                                                                                                                                                                     3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCATGAAATCTC 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCATAÁAÁTCCC 1723
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                                                                                                                                                                                                                                                                                     3.9%
Best Local Similarity 86.0%
Matches 166; Conservative
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1796

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Sequence 2000 BP; 648 A; 369 C; 364 G; 619 T; 0 U; 0 Other;

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soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; soorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
                                                                              Plant; gene; 88; transcription; plant genome augmentation; cereal;
                                                                                                                                                                                                                                                                                                                                  T, Briggs SP, Cooper B, Glaz
Kreps J, Provart N, Ricke D,
               ADJ40707 standard; cDNA; 2000 BP
                                                                                                                                                                                                   26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
                                                                                                                                                                                    26-SEP-2002; 2002US-00260238
                                               06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                   Moughamer
                                                                                                                                                                                                                                                                 GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                          Goff SA, Katagiri F,
                                                                                                                                                                                                                                  BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-190374/18.
                                                                                                                                                                                                                                                                                           KREPS J.
PROVART N.
RICKE D.
                                                              Plant cDNA #1707.
                                                                                                                                                    US2004016025-A1.
                                                                                                                                                                                                                                                                                                                   ZHU T
                                                                                                                                                                    22-JAN-2004
                                                                                                                     antifungal
                                                                                                                                      Eukaryota
                               ADJ40707;
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(RICK/)
(ZHUT/)
                                                                                                                                                                                                                                    (BUDM/)
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                                                                                                                                                                                                                                                                                   (KATA/)
                                                                                                                                                                                                                                                                   (GLAZ/)
                                                                                                                                                                                                                                                                           GOFF/
RESULT 8
ADJ40707
ID ADJ40
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New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.

Glazebrook J; e D, Zhu T;

Claim 26; SEQ ID NO 1707; 230pp; English.

The invention relates to plant nucleotide sequences that direct seed-,

leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential

or constitutive transcription of an operatively linked nucleic acid

segment. The invention also relates to a method for augmenting a plant

genome and a method of identifying a gene, where its expression is

altered in the seed, leaf, stem, panicle, pollen, root or is constitutive

in a plant cell. The plant is a creal, e.g. soybean, alfalfa, sunflower,

canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

sorghum, rice or wheat. The polynucleotides and the polypeptides they

encode are useful for manipulating crop plants to alter or improve

phenotypic characteristics, to produce large quantities of oil or

chencypic characteristics, to produce large quantities of oil or

chencypic characteristics, consecticides, viruses or fungi, and to

incur stress tolerance (e.g. salt, cold or drought) to ensure the plants

chave a high nutritional value with reduced apical dominance or dwarfism,

canly incur stress tolerance (e.g. salt, reduced apical dominance or dwarfism,

canly flowering or altered metabolic pathways. This sequence represents a

canly incleic acid of the invention. Note: The sequence data for this

can electronic format directly from USPTO at sequence.

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                                                                                                                                                                   491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used to screen substrates, drugs or compounds which modulate ICK activity and treat disorders characterized by an insufficient or excessive production
                                                                  2446 AAACATAAAGGGTTAAATGCATGGTAGGCTCTTGATCTTGTCTGGAGGTGCCACTTAGGT
                                                                                                                                                                                                                                                                   2506 CCACAAACTCTCAAATTGCATTTTTGACACCCTAATGTTATTCAAGTGTGCCACTTAGAT
                                                                                                                                                                                                  CTACAAACTCTCAAAATGCATTTCTGATACCCTAGTGTTGTTCAAGTGTGTCACTTAGGC
                                                                                                                                                                                                                                  492 C--CCAAATCACTAAAACCTCTTCAGGTTCTTACGTGACGTTGATGTGTATGCCTCACGG
                                                                                                                                                                                                                                                                                                    372 AAAATTCAAGAGTAAAGTGTACGGGCAGTCTTTAAACTTGTAGGGGTATGTCTTCTAGAT
                                                                                                                                                                 432 CCCTAAACTCTCAAAATGCATATCCAAGTCCCATAACTTGTCATAGTGTGCCATCTAGGT
                                    Gaps
2.2%; Score 66.8; DB 12; Length 2000; 56.7%; Pred. No. 1.7e-07; ive 0; Mismatches 107; Indels 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant; ds; gene; inhibitor of cyclin dependent kinase; ICK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding broom corn ICK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 41; Page 125; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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Hatzfeld Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK93956/c
ID ABK93956 standard; DNA; 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-2001; 2001WO-IB001492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUL-2000; 2000US-0218471P.
13-OCT-2000; 2000US-0241219P.
                                                                                                                                                                                                                                                                                                                                     2686 GAACTAGTTGAT 2697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                    610 CTTTŤCTŤTÀT 621
                                  Conservative
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                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICK inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABG65676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorghum bicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200228893-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-2002
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                               Matches 143;
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 Query Match
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                                                                                                                                                                                                                  ATACTTAGTTAGTATCATAATTATTATTATTATAATATAAATTTGGTCAAACTTAGAA 632
ICK wild type protein. The present sequence represents a cDNA molecule encoding an inhibitor of cyclin dependent kinase (ICK) protein of the invention
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                    1400 GC-TTTGACTCTTCAAGATTCTTGGAATGACTTATCATTTGGGGTAGGGAG 1449
                                                                                                                                                                                                                                                                                          631 AAGTITGACTCTCCAAGAITCTTGTAATGACTTACAAITTGGAATGGAGAG 581
                                                                                                                                                     1;
                                                                                                             Score 65.4; DB 6; Length 1334; Pred. No. 3.3e-07;
                                                                           Sequence 1334 BP; 303 A; 337 C; 376 G; 318 T; 0 U; 0 Other;
                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize oil-associated gene genomic amplicon #4.
                                                                                                   2.2%; bcc. No. 5...
80.2%; Pred. No. 5...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  ADJ48000 standard; DNA; 701 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                     89; Conservative
                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ48000;
                                                                                                                 Query Match
                                                                                                                                                       Matches
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ds; maize; plant; oil-associated gene; transgenic; enhanced seed oil; vegetable oil. Rogers JA; 15-MAR-2002; 2002US-0365301P. 26-JUN-2002; 2002US-0391786P. 26-JUN-2002; 2002US-0392018P. 14-MAR-2003; 2003US-00389566 LAURIE C C. RAVANELLO M. SAVAGE T. LEDEAUX J R. (LAUR/) LAURIE C C. (RAVA/) RAVANELLO M. (SAVA/) SAVAGE T. (LEDE/) LEDEAUX J R. (ROGE/) ROGERS J A. US2004025202-A1. 05-FEB-2004. Zea mays. RESULT 10
ADJ48000/
XXX
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DE ADJ49
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Ledeaux JR, Savage T, Laurie CC, Ravanello M, WPI; 2004-142683/14. Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic

Example 1; SEQ ID NO 4; 22pp; English.

plant seed

promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgent plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents a maize oil-The invention relates to a recombinant DNA construct comprising a associated gene genomic amplicon.

Sequence 701 BP; 230 A; 119 C; 115 G; 237 T; 0 U; 0 Other;

Query Match

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2.1%; Score 62; DB 12; Length 701;
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The invention relates to a corn seedling-derived polynucleotide (cdp)

selected from ADS64985-ADS71316, or their complements and fragments. Also
included are a composition for the detection of altered expression of a

cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a

method of detecting a polynucleotide in a biological sample using a cdp,

c method for using oligomers (and amplification) to recover a regulatory

element from a DNA library using oligomers designed against a cdp, a

seedling specific regulatory element that regulates the expression of a

cdp, an expression vector containing a cdp or regulatory element, a plant

transformed with the vector, a host cell containing the vector (and

expressing a compound which binds a CDP and screening a plurality of

cdentifying a compound which binds a CDP and screening a plurality of

compounds for binding to cdp polynucleotide. The cdp polynucleotides,

proteins, vectors, cells and antibodies are useful for the

identification, evaluation and alteration of seed growth and development,
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                                                             1340 ACATTTAGTTGGTATCATAAATATTATTATTATCATATAAATTTGATC-AACTTGAGA 1398
                                                                                                                                              1399 TGCTTTGACTCTTCAAGATTCTTGGAATGACTTATCATTTGGGGTAGGGAGTAGGTTTCT 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth; seed development; disease resistance; insect infestation; fungal disease; bacterial infection; Goss Bacterial Wilt; blight; Stewart's bacterial wilt; Holus spot; bacterial leaf blight; leaf spot; bacterial stripe; maize dwarf mosaic virus infection;
                                                                                                     549 ACGITITATITIAATATATATATATITATITATITATIATAAATITIGGTCAAACTIGATA 490
                                                                                                                                                                                      489 recrircarriccaaaaagrircaarricarriararricacaaccadagarricadaga 430
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                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         environmental stress; water stress; pH stress; temperature stress;
pollution; injury; pesticide.
                     ;
  Pred. No. 2.1e-06;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corn seedling-derived polynucleotide (cpds), SEQ ID 3721.
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                                                                                                                                                                                                                                                                                                                                                                                 BP.
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99US-00298329.
                                                                                                                                                                                                                                                                                                                                                                                 ADS68705 standard; cDNA; 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-2001; 2001US-00923876.
1 Similarity 72.3%;
94; Conservative
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                                                                                                                                                                                                                                    1459 AAGGCCAGTC 1468
                                                                                                                                                                                                                                                                            429 AAATACAGTC 420
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    Best Local Similarity
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                          Matches
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             infection, Goss' Bacterial Wilt, blight, Stewart's bacterial Wilt, Holcus spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf mosaic virus infection) and resistance to environmental stress (e.g. water stress, pH stress, tensorature stress, pOllution, injury or pesticides. The present sequence is cdp cDNA sequence.
 bacterial
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                                                                                                                                                       2.0%; Score 61.2; DB 7; Length 290; 71.1%; Pred. No. 2.1e-06; tive 0; Mismatches 33; Indels (
                                                                                                                     Sequence 290 BP; 58 A; 113 C; 75 G; 43 T; 0 U; 1 Other;
                                                                                                                                                                                              Conservative
                                                                                                                                                                             Local Similarity
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ADA72001 standard; DNA; 2000 ADA72001; RESULT 12

20-NOV-2003 (first entry) Rice gene, SEQ ID 5326

Plant; bacterial infection; fungal infection; viral infection; rice; dB. dene;

Oryza sativa

WO2003000898-A1

03-JAN-2003

22-JUN-2001; 2001WO-IB001105

22-JUN-2001; 2001WO-IB001105

(SYGN) SYNGENTA PARTICIPATIONS AG

ö Hou Y; SA, Hou Zhu T, Glazebrook J, Goff Whitham S, Xie Z, ч, Cooper S. Tao Chen W, Co F, Quan S, Katagiri F, Chang

WPI; 2003-175290/17.

Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression

Claim 27; SEQ ID NO 5326; 899pp; English

involved in plant resistance or response to pathogenic infection. Micomprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to does not expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance to a plant to fungal or viral infection. The present sequence was used to present invention relates to a method (M1) for identifying genes bacterial, iungal or vira. illustrate the invention. bacteria]

Sequence 2000 BP; 708 A; 348 C; 340 G; 604 T; 0 U; 0 Other;

Length 2000;

DB 8;

Score 60.4;

2.0%;

Query Match

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2490
                                                                                                                                  2491 AGGTGCCACTTAGGTCCACAAACTCTCAAATTGCATTTTTGACACCCTAATGTTATTCAA 2550
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                                                                                                                                                                   646 GTGTGTCACCTACGTCCATAAACTCTTAAAATGTATTTTTGGATCCGTCGTACTTATCTC 587
                                                                                                706 AACTICCICICAAAAAAAACTITTAGACTAAAGTGCATGGGTGGTCCATAAACTIGTACGG
                                                               2431 AAGTCGACCACAACCATAAAGATTAAATGCATGGTAGGCTCTTGATCTTGTCTGG
                              Gaps
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                              Indels
            Pred. No. 1.1e-05;
0; Mismatches 56;
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62.7%; PL.
          Similarity 62.7
94; Conservative
                             94;
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            Best Local
Matches 9
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plant biotechnology; carbohydrate synthesis; carbohydrate metabolism; exbohydrate degradation; carbohydrate; plant grain; grain filling; corn; tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain; Rice DNA sequence Seq ID868 related to grain filling. (first entry) gene; ds; plant 18-DEC-2003

RESULT 13 ADCO8563/c ID ADC08563 standard; DNA; 2010

ADC08563;

Oryza sativa.

WO2003000905-A2

3-JAN-2003.

21-JUN-2002; 2002WO-IB002450.

22-JUN-2001; 2001US-0300112P. 26-SEP-2001; 2001US-0325277P. 20-DEC-2001; 2001US-0342327P.

SYGN) SYNGENTA PARTICIPATIONS AG.

Moughamer Ricke D; Cheng W, Briggs S, Cooper B, Goff SA, ok J, Katagiri F, Kreps J, Provart N, Glazebrook J,

WPI; 2003-229341/22.

New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.

Disclosure; SEQ ID NO 868; 130pp; English.

This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nucleotide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, ever, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is a DNA sequence of a rice gene promoter. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences.

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WO2003000905-A2
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Best Local 8
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                                                                                                                                                                                                                                                                         2554 TGCCACTTAGATCTACAAACTCTCAAAATGCATTTCTGATACCCTAGTGTTGTTCAAGTG
                                                                                                                                                                                                                                                                                                                                                   2614 IGICACITAGGCAAGAAAAGITAGAIAAITITGA-TAAGCIATGGGACCAAAITAAITITA
                                                                                                              2434 TCGACCACAACCAAACATAAAGAGTTAAATGCATGGTAGGCTCTTGATCTTGTCTGGAGG
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                                                                             Gaps
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e D, Zhu T;
                                  2.0%; Score 59; DB 10; Length 2010; 58.0%; Pred. No. 2.7e-05;
563 A; 472 C; 389 G; 586 T; 0 U; 0 Other;
                                                                           0; Mismatches 100; Indels
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ps J, Provart N, Ricke D,
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Goff SA, Katagiri F, Kreps J,
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26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
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                                                                           Matches 141; Conservative
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MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
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PROVART N.
RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ41371 standard;
                                                       Local Similarity
Seguence 2010 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      679 TTT 677
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                                    Query Match
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(RICK/)
(ZHUT/)
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(GOFF/)
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ADJ 41
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The invention relates to plant nucleotide sequences that direct seed., leaf- and/or stem., panicle., root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polymucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants of the plants of the continuous or source or dwarfism, and to all the continuous or source or continuous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2567
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New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             early flowering or altered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          885 AAAAATAGAGTAAAGTCCATCACCGGTCCCTAAACTTGTACTGTTGTGTCATCGCGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2000 BP; 662 A; 359 C; 368 G; 609 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2371; 230pp; English
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Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Glazebrook J, Katagiri F, Kreps J, Provart N,
                                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS AG.
22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
                                                                                                                                                                                                                                                                                 WPI; 2003-229341/22.
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Moughamer T; Ricke D;

This invention, in the area of plant biotechnology, relates to novel
polynucleotides comprising a nucleotide sequence encoding a protein which
is involved in or associated with the synthesis, metabolism or
degradation of carbohydrates in the plant grain and the expression of
which is up-regulated during grain filling. The plant is selected from
corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
sugarbbet, wheat, and rice. The invention may be useful for the
improvement of protein, oil, starch, fibre and moisture content of the
cereal grains. In addition, carbohydrate levels may be modified to a more
desirable level using the present invention. The present sequence is a
DNA sequence of a rice gene promoter. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at

Etp.wipo.int/pub/publishedpct_sequences. New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties. Disclosure; SEQ ID NO 868; 130pp; English. R R R X R X R I I I X R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R I K R

Score 53.4; DB 10; Length 2010; Pred. No. 0.001; 0; Mismatches 41; Indels 0; Sequence 2010 BP; 563 A; 472 C; 389 G; 586 T; 0 U; 0 Other; Query Match 1.8%; Best Local Similarity 65.5%; Matches 78; Conservative (

2455 GAGTTAAATGCATGGTAGGCTCTTGATCTTGTCTGGAGGTGCCACTTAGGTCCACAAACT 2514 2515 CTCAAATIGCATTTTTGACACCCTAATGTTATTCAAGTGTGCCCACTTAGATCTACAAAC 2573 427 CCCAAAATGCATTCCAGGTCCCCAGAACTTATCAAAGTGTATCATCTAGGTCCCAAAATC 485 ઠ g ઠે a

0; Gaps

Search completed: February 16, 2005, 04:09:58 Job time : 1555 secs

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Sequence 10, Appl
Sequence 3, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 22, Appli
Sequence 22, Appl
Sequence 2813, Ap
Sequence 2813, Ap
Sequence 15974, A
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14720, A
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10071.450 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                  February 16, 2005, 02:54:17 ; Search time 490 Seconds
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/RDGUSB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/1/ina/pcTuS COMB.seq:*
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-6946/A-10
US-09-693-46/A-10
US-09-866-153-3
US-09-866-153-3
US-09-866-153-3
US-09-866-153-8
US-09-866-153-8
US-09-86-153-8
US-09-86-153-8
US-09-806-708B-22
US-09-806-708B-22
US-09-806-708B-22
US-09-806-708B-22
US-09-949-016-15974
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US-08-999-116-1137
US-08-999-416-1137
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US-09-631-976-15639
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US-09-949-016-107633
US-09-949-016-107633
US-09-949-016-107633
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US-09-998-416-288
US-09-998-416-288
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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3016
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Match Length
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                                                        Sequence 14543, A Sequence 12557, A Sequence 13137, A Sequence 9644, Ap Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 12876, A Sequence 13871, A Sequence 3, Appli Sequence 3, Appli
    118, App
2, Appli
14095, A
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Sequence 10, Application US/09866153

Sequence 10, Application US/09866153

Sequence 10, Application US/09866153

Sequence 10, Application US/09866153

GENERAL INFORMATION:
APPLICANT: Mal. Halrong

TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF

CURRENT APPLICATION NUMBER: US/09/866,153

CURRENT PILING DATE: 2001-06-24

PRIOR FILING DATE: 1999.03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1795 TTTACGAAGATGAAACTCTTCCTGCACTGTTTTCCAAATATGGGTTGCATTAATAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1914 AGTTTTCTGAGGCCCGTCTCAGF-GGATTTCATCAGAGTTTCATGACATTAAATAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG
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                                                                                                                                                                                                                                                                                                                                     Sequence 40,
                        Sequence
                                                                                                                                                                                                                                                                                                                   Sequence
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COTHER INFORMATION: The "n" at position 9 is any nucleotide US-09-866-153-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.9%; Score 118.6; DB 4; Length Best Local Similarity 86.0%; Pred. No. 1.3e-25; Matches 166; Conservative 0; Mismatches 24; Indels
US-08-781-986A-118
US-08-749-522-2
US-09-949-016-14543
US-09-949-016-14543
US-09-949-016-13137
US-09-949-016-13137
US-09-248-796A-9644
US-08-949-016-13137
US-08-990-571-8
US-09-559-098A-8
US-09-559-098A-8
US-09-569-016-13871
US-09-949-016-13871
US-08-845-258-3
US-08-845-258-3
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US-08-845-258-3
US-08-949-016-13871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Saccharum Hybrid Cultivar 32-8560
                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-693-467A-10/c
; Sequence 10, Application US/09693467A
; Patent No. 6686513
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 3688
  NAME/KEY: misc_feature
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SEQ ID NO 3
LENGTH: 3691
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APPLICANT: Albert, Henrik H.
APPLICANT: Wei, Hairong
TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
FILE REFERENCE: UH-03648
CURRENT APPLICATION NUMBER: US/09/270,976A
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 3688
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APPLICANT: Albert, Henrik H.
APPLICANT: Albert, Henrik H.
APPLICANT: Wei, Hairong
TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
TITLE REPERENCE: UH-04331
CURRENT APPLICATION NUMBER: US/09/693,467A
CURRENT FILING DATE: 2000-10-20
PRIOR PAPLICATION NUMBER: 09/270,976
PRIOR PAPLICATION NUMBER: 09/270,976
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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; OTHER INFORMATION: The "n" at position 9 is any nucleotide
(08-09-270-976-10
                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (9) 7

COTHER INFORMATION: The "n" at position 9 is any nucleotide. US-09-693-467A-10
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Pred. No. 1.3e-25;
0; Mismatches 24; Indels
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ORGANISM: Saccharum Hybrid Cultivar 32-8560
                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Saccharum Hybrid Cultivar 32-8560
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; Sequence 10, Application US/09270976A
; Patent No. 6706948
; GENERAL INFORMATION:
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Best Local Similarity 86.0%;
Matches 166; Conservative
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Matches 166;
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1451 AGGITTCTAAGGCCAGICTCAGIGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT 1510
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APPLICANT: Albert, Henrik H.
APPLICANT: Albert, Hairong
TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
FILE REFERENCE: UH-0431
CURRENT APPLICATION NUMBER: US/09/693,467A
CURRENT FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Malerik H.
APPLICANT: Wel, Halrong
TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
TITLE OF INVENTION: PLANT PROMOTER: US/09/866,153
CURRENT APPLICATION NUMBER: US/09/866,153
CURRENT PILING DATE: 2001-05-24
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 1.3e-25;
0; Mismatches 24; Indels 3;
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OTHER INFORMATION: The "n" at position 9 is any nucleotide.

NAME/KEY: misc feature

LOCATION: (3613)

OTHER INFORMATION: The "n" at position 3613 is any nucleotide.

US-09-866-153-3
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ORGANISM: Saccharum Hybrid Cultivar H32-8560
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                                                                                                                                                                                                                                                                                                                                                                    US-09-866-153-3/c;

Sequence 3, Application US/09866153;

Patent No. 6638766;

; GENERAL INFORMATION:
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Best Local Similarity 86.0%;
Matches 166; Conservative
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (9)
UNTER INFORMATION: The "n" at position 9 is any nucleotide.
NAME/KEY: misc_feature
LOCATION: (4318)
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OTHER INFORMATION: The "n" at position 4318 is any NAME/KEY: misc feature
LOCATION: (4546)
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ORGANISM: Saccharum Hybrid Cultivar H32-8560
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Patent No. 6638766
GENERAL INFORMATION:
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OTHER INFORMATION: The
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LOCATION: (5125)
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Best Local Similarity
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Patent No. 6706948

Patent No. 6706948

Patent No. 6706948

Patent No. 6706948

APPLICANT: Mei, Henrik H.

APPLICANT: Wei, Hairong

TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF FILE REFERENCE: UH-03648

CURRENT APPLICATION NUMBER: US/09/270,976A

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 3691
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Pred. No. 1.3e-25;
0; Mismatches 24; Indels 3;
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NAME/KEY: misc feature

LOCATION: (3013)

OTHER INFORMATION: The "n" at position 3613 is any nucleotide.

US-09-693-467A-3
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OTHER INFORMATION: The "n" at position 9 is any nucleotide
                                                                                                                                                                                                                                                        "n" at position 9 is any nucleotide
                                                                                                                                         TYPE: DNA ORGANISM: Saccharum Hybrid Cultivar H32-8560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Saccharum Hybrid Cultivar H32-8560
PRIOR APPLICATION NUMBER: 09/270,976
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 3691
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Best Local Similarity 86.09
Matches 166; Conservative
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                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (9)
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1571 ȚȚCATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Albert, Henrik H.
APPLICANT: Wei, Hairong
APPLICANT: Wei, Hairong
TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
FILE REFERENCE: UH-03648
CURRENT APPLICATION NUMBER: US/09/866,153
CURRENT APPLICATION NUMBER: 09/270,976
PRIOR APPLICATION NUMBER: 09/270,976
PRIOR FILING DATE: 1999-03-17
SNOWHARE OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VET. 2.0
1855 GATGTGGCACCGTATTGATGATGAGAGAGAGATGATAAGAGTTTCATGGAATTAGAGAGT
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86.0%; Pred. No. 1.6e-25;
tive 0; Mismatches 24; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (4890)
OTHER INFORMATION: The "n" at position 4890 is any nucleotide.
NAME/KRY: misc feature
LOCATION: (5117)
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NAME/KEY: misc feature
LOCATION: (5150)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at position 5117 is any nucleotide
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RESULT 9
US-09-270-976-8/c
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                                                                               RESULT 8
US-09-633-467A-8/C
US-09-633-467A-8/C

J Sequence 8, Application US/09693467A
Patent No. 6686513
GENERAL INFORMATION:
APPLICANT: ALBERT, Henrik H.
APPLICANT: Wel, Halrong
TITLE OF INVENTION: PROMOTER SEQUENCES AND METHODS OF USE THEREOF
FILE REFERENCE: UH-04331
CURRENT APPLICATION NUMBER: US/09/693,467A
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/270,976
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1855 GATGTGGCACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGGAATTAGAGAGT 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1795 TTTACGAAGATGAAACTCTTCCTGCACTGTTTTCCAAATATGGGTTGCATTAATAACATG 1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1914 AGTTTTCTGAGGCCCGTCTCAGT-GGATTTCATCAGGAGTTTCATGGACATTAAATAGGCT
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: DCATION: ($150)

; DTER INFORMATION: The "n" at position 5150 is any nucleotide

US-09-693-467A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (9)
OTHER INFORMATION: The "n" at position 9 is any nucleotide.
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Pred. No. 1.6e-25;
0; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at position 5117 is
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Saccharum Hybrid Cultivar H32-8560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 86.0%;
Matches 166; Conservative
1629 GCCATGAAATCTC 1641
                               1735 GCCATAAATCCC 1723
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LOCATION: (4546)
OTHER INFORMATION: The
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LOCATION: (4890)
OTHER INFORMATION: The
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LOCATION: (5125)
OTHER INFORMATION: The
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OTHER INFORMATION: The
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OTHER INFORMATION: The
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LOCATION: (9)
                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 8
LENGTH: 5174
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NAME/KEY:
LOCATION:
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1855 GATGTGGCACCGTATTGATGATGAGAGAGAGATGATAAAGAGTTTCATGGAATTAGAGAGT 1796
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Sequence 8, Application US/09270976A

Sequence 8, Application US/09270976A

Patent No. 6706948

GENERAL INFORMATION:
APPLICANT: Albert, Henrik H.
APPLICANT: Wei, Hairong

TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF

TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF

CURRENT APPLICATION NUMBER: US/09/270,976A

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 5174
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OTHER INFORMATION: The "n" at position 5125 is any nucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
i LOCATION: (5150)
corner INFORMATION: The "n" at position 5150 is any nucleotide.
US-09-270-976-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at position 4318 is any nucleotide
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3.9%; Score 118.6; DB 4; Length Ebest Local Similarity 86.0%; Pred. No. 1.6e-25;
Matches 166; Conservative 0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at position 9 is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at position 4890 is
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Saccharum Hybrid Cultivar H32-8560
FRATURE:
LOCATION: (9)
OTHER INFORMATION: The "n" at position 9 is $\varphi$
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US-09-806-708B-22
; Sequence 22, Application US/09806708B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1629 GCCATGAAATCTC 1641
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LOCATION: (4318)
OTHER INFORMATION: The "n"
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NAME/KEY: misc_feature
LOCATION: (5117)
OTHER INFORMATION: The "n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (4546)
OTHER INFORMATION: The "n"
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NAME/KEY: promoter

LOCATION: (1)..(1141)

OTHER INFERMATION: consensus sequence of A.t., L.a., and B.n. FAEI promoters
US-09-806-708B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1038 TAACCTCTCTGTTTCCATCGTCCTCTAACCGCGAAGAGCGGACGCACAAGACTTAGAGTC 1097
2743 TGTATAGTACTAGCTAGTATAACTTTTTCAAGTTGTAGCTACTTATAGCTTATACTCC 2802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1093 TAWWTNHAKRGATMCWYWYGTNRRWCMRTYAMRTWYTRSNANWSCATKBMWWTMKWYA 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   973 MYGAAAGIKWGCMAAMATMGBWWADTAGKMCNNNNNWTTDVRRMAMKAKNNNNNAYWT 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               918 GCATGAGTGCACCGTTCGTCCGCGGGTTCCTTTTCTCGTGGTGCCGTGCACGCCTCTGCGT 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              853 WANAWWIRINNNNNNNNNNACRNIRIWWABWKHSWCNNNNNNNNNNNNNNNNTWCHYITANA 794
                             GCTGAAATCGACCGGCCGGGCCGACCAACAGGAGGTCAGCTCGGCCACTCCGTCTCCGAGC 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             913 ACYNRAATHNNKMATHWMKWTHGAHSKRRTRHHTRTCRRTKYNNNNNARTVYWYHHAARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    678 TATCTCTAAAGGGGAACGAATGGATGGTGGACACGTGTGGGGGACACCGAAGGGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                    GENERAL INCORNATION:
APPLICANT: The University of British Columbia
APPLICANT: The University of Embryonic Transcription in Plants
TITLE OF INVENTION: REGulation of Embryonic Transcription in Plants
FILE REPERENCE: 481.0-58741
CURRENT PAPPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR PILING DATE: 1999-08-04
NUMBER: OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
                                                                                            2803 GCATATTACAATCAAATAGAATTCGGAAGTACTATAAACGGGAGCCTATA 2852
                                                                                                                            904 NNATIYNRGTAWRINNNNNMTMKTKYYBHAAWNNNNNGKMCTAHTWWV 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.5%; Score 46; DB 4; Length 1141; Best Local Similarity 11.3%; Pred. No. 0.0033; Matches 115; Conservative 352; Mismatches 546; Indels
                                                                                                                                                                                                                                                            Sequence 22, Application US/09806708B Patent No. 6784342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                 RESULT 11
US-09-806-708B-22/c
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LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2143 TACAATATGAGATTTCATCTAAGAGCCAACACCTGACTGGTACTGTTGAAGGTGTCCTAG 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGAGTGGTCGATCTTTTAGTTGTTAGTAGTGTAAGACCTAGTTTAGTGCTCTTTTCTT 2262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAATTCTAAAATGATGCCAAATAAAGATAGATTACAAAGTTAAACGACGGAAAAACTCT 2382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 GGTCCACAAACTCTCAAATTGCATTTTTGACACCCTAATGTTATTCAAGTGTGCCACTTA 2562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCTACAAACTCTCAAAATGCATTTCTGATACCCTAGTGTTGTTCAAGTGTGTCACTTA 2622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2263 GTCTAGGTTTATGTTGTGTTTTGGCTGCCAAGTGTTGAACAACTCAAGGTAAGGTCCCAT 2322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 YTKSSWNYTSRYYRWKTNNSWRWRSDTRSMGRANNYARABHYGYKWNTRWBWSHTWBHB 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 WRAMBDTVDHHYVTAMNNAWTIMCMMDKDDKRTRWWWKKONNATGWDDDTKYHMMNNGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 WHSAWKKWHANAAHYSRKKWTBYKRKTWVNNNNGTTWWKRMWAWYWKMDMDWBGTYNNNN 429
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              GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REPERENCE: 4810-58141
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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1 Similarity 9.8%; Pred. No. 0.00029;
81; Conservative 311; Mismatches 432;
                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMA
US-09-806-708B-22
                                                                                                                                                                                                                                                                                  LENGTH: 1141
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1353 ATCATAAATATTATTATTATCATATAAATTTGATCAACTTGAGATGCTTTGACTCTTC 1412
                                                                                                                                           AAGATTCTTGGAATGACTTATCATTTGGGGTAGGGAGTAGGTTTCTAAGGCCAGTCTCAG 1472
                                                                                                                                                                                                                    1473 TGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATGTGACACCGTATTGATGAA 1532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1158 ATCATGTCGACCGGCACGTTTAATATTTAACTTATACCATATGAATATCATGTCGAACTA 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 ASCMMRRKYAGKSKTSYKSMMMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 WWWGKARKWSTWRKSRSYASARSAKRCCYSCSWGAMSWXYWWRWRWRGWATGAGMKAWR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 YMWKRWWWCWARMYRYSTGTRASMWWRRWYYTMMMKWWKYAWARAAWRWAMWAMRARRAC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 MCWWWGRWWSTYWYMAWGKKWWRYATTWRRAMMWWAAATWWWYMWAAWTWRAAMYR
                                                                                                                                                                     5 WWKYTTWYAKCWTKWKWSWSYMNYWKWYYMKTYWRWRRKKKKKAWWKYWKTWTWWWYWRYAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 1.4%; Score 41.2; DB 4; Length 8 I Similarity 12.0%; Pred. No. 0.085; 46; Conservative 164; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054R2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
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                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2813, Application US/09621976
; Patent No. 6639063
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ORGANISM: Homo sapiens
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; LOCATION: 235..399
US-09-621-976-2813
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TGAGGATGATACTTTTCTGAACGTGATTGCGTGAGTTATTAAATTGTACTTTTAGTTGTT 1277
                                                                                                                                                       CTACATTTAGTTGGTATCATAAATATTATTATTATCATATAAATTTGATCAACTTGAG 1397
                                                                                                                                                                                                                                ATGCTTTGACTCTTCAAGATTCTTGGAATGACTTATCATTTGGGGGTAGGGAGTAGGTTTC 1457
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                                                                                                 254 TBKRNYKYCYAYB-WYYBMYMGKHHWBWWRRABHRSWNMWWVKCRNKYMVSWHYHAMRYB 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 KWABAVGCNNNWKDRMAHHHWCATNNNMMWWYAYMFHMHKKGKAAWTNNKTABRDDHBA 136
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APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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Patent No. 6519063
PERERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
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ORGANISM: Homo sapiens
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Best Local Similarity
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; LOCATION: 235..399
US-09-621-976-2813
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US-09-621-976-2813/c
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Sequence 150744, Application US/09949016
Fatent No. 6812339
GENERAL INFORMATION:
FATENCE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PELING DATE: 2000-04-14
FRICH FILING DATE: 2000-10-20
FRICH FILING DATE: 2000-10-03
FRICH APPLICATION NUMBER: 60/231,498
FRICH APPLICATION NUMBER: 60/231,498
FRICH FILING DATE: 2000-09-08
FRICH FR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 AGCACTIGIATIGCIACCATITICATITIAGCCACIGIGATAGATATGTATCTCATIGTGC 229
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1.4%; Score 40.8; DB 4; Length 60
Best Local Similarity 48.3%; Pred. No. 0.088;
Matches 114; Conservative 0; Mismatches 122; Indels
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| LCCATION: (1)...(294836)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15974
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ORGANISM: Human
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Search completed: February 16, 2005, 10:31:38 Job time : 494 secs

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NAME/KEY: TATA_signal
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Sequence 151068,
Sequence 19630, A
Sequence 10, Appl
Sequence 3, Appli
Sequence 8, Appli
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Sequence 10015, A
Sequence 42192, A
Sequence 32756, A
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| Cgn2_6/ptodata/2/pubpna/US06_WWW_PUB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/DS06_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_WWW_PUB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-767-701-19690

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US-10-767-701-11451

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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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3016
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No.
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Sequence 183742, Sequence 24208, A Sequence 142566, Sequence 165368, Sequence 7017, Ap Sequence 7017, Ap Sequence 1701, Ap	27759, 27759, 25020, 4, App 25018, 31959,	6 3721, 7 6 124251 6 42140, 8 6 517, A 6 53393, 8 6 183742 6 183742	Sequence 62353, A Sequence 62353, A Sequence 95392, A Sequence 95390, A Sequence 17495, A Sequence 2371, Ap Sequence 42065, A Sequence 31961, A Sequence 30623, A Sequence 30633, A Sequence 30623, A
US-10-425-115-183742 US-10-425-114-24208 US-10-425-115-142566 US-10-425-115-165368 US-10-767-701-10788 US-10-767-701-10788 US-10-260-238113113	10-333-006-7 -10-425-114-2775 -10-425-115-2502 -10-389-566-4 -10-437-3195	5.09-923-876-372 5.10-425-114-356 5.10-425-115-124 5.10-437-963-617 5.10-437-963-533 5.10-425-114-327 5.10-425-114-351 5.10-425-114-351	US-10-767-701-24985 US-10-437-963-62353 US-10-437-963-93872 US-10-437-963-95390 US-10-437-963-17495 US-10-260-238-2371 US-10-437-963-42065 US-10-437-963-31961
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ALIGNMENTS

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SQUENCE 1. APPLICATION US/10751612

SQUENCE 1. APPLICATION US/10751612

PUBLICATION NO. US2005000532A1

GENERAL INFORMATION:

SAPPLICANT: MIXOV, T. Erik

APPLICANT: Reddy, Avutu,

APPLICANT: Email, Chandrakanth,

APPLICANT: MUMBER: US/10/751,612

CURRENT APPLICATION NUMBER: US/10/751,612

CURRENT PELING DATE: 2003-01-03

FILE REPERENCE: 017575-0774

CURRENT PELING DATE: 2003-01-03

NUMBER: OF SEQ ID NOS: 1

SOFTWARE: FastSEQ for Windows Version 4.0

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10.1 GANGGOCCTCTGGGTTCACCGGGAACCATCAGAACGTTCCCCTTTTACAGGG 1020 1021 GANGGOCCTCTGGGAACCCGCTGAAACCCATCAGAACGGCCCT 1030 1021 GANGGOCCTCTGGAAGCCGCTCTGCTTCACAGGCCGGCC 1030 1021 GANGGOCCTCTGAAGCTCTTTTTTTTTTTTTTTTTTTTTTTTT	2041 CTAACGTGAAGAGAGAGCTATTTTTTTTTGCTCCCCAATACATGATAGATA
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Page 3

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: 105/163222)B

CURRENT APPLICATION NUMBER: US/10/425,115

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 151068

LENGTH: 576

TYPE: N.
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; Sequence 19690, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongue
; APPLICANT: Cao, Yongue
; APPLICANT: Cao, Yongue
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(51535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 19690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 TTCTGGGTACCCGCGCAGAATCGCCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cch 4.0%; Score 120.8; DB 18; Length al Similarity 66.9%; Pred. No. 5.5e-22; 198; Conservative 0; Mismatches 77; Indels
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US-10-767-701-19690
                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: MRT4577_69292C.1
US-10-425-115-151068
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ORGANISM: Zea mays
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US-10-767-701-19690
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                                                                                                                                                  CTAAGAGCCAACACCTGACTCGTACTGTTGAAGGTGTCCTAGTTGGAGTGGTCGTTCTTT
                                                                                                                                                                                                                                                                                                                                 TAGITGITAGIGIAAGACCIAGITTAGIGCICTITTCTTGICTAGGITTATGITGI
                                                                                                                                                                                                                                                                                                                                                                            2221 TAGTIGITAGIAGICIAAGACCIAGITIAGICCICITITICITGICIAGGITIATGITGIG
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                                                                                                                                                                                                                                       CTAAGAGCCAACACCTGACTCGTACTGTTGAAGGTGTCCTAGTTGGAGTGGTCGATCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGICAAGICCAIGG 3016
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US-10-425-115-151068
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460 496 363 397

338 TTCTGGGTACCCGCGGAGAATCGGCCTCCATGTAGTTAGCCTCGTCAGGCATGGGGGGAA

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LOCATION: (5117)
OTHER INFORMATION: The "n" at position 5117 is any nucleotide.
NAMB/KEY: misc_feature
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PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 3691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (9)
OTHER INFORMATION: The "n" at NAME/KEY: misc feature
LOCATION: (4318)
OTHER INFORMATION: The "n" a' NAME/KEY: misc_feature
LOCATION: (4546)
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LOCATION: (5117)
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Matches 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TICATGGGGATGAAACTCTT-CTTCACTGTTTCCAAAATAT-AGATGCATTGGTAAGAGG 1628
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                                                                                                                                                                                                            484 GAATTGGGTGAGATTGAGAGAAACGAGAAGAAGAATGCTAATCTAATTACCCTTCCGTAT 543
                                                            -GTCGTCAGGCATGGAGA 436
                                                                                                                                                                   GTACTGGCTGAGATGCCATTGTTGTGTAGATCGAGAAACGAGAAGAATGCTAGTCTAA 496
        364 CICTGGGTACATGAGAGAATCGTCTTCCATGTGGTTTGCCTCGTCAGGCATGGGGGAA 423
                                                                                                              TTGGCTGAGATGCCCCCGTATAGCTGGTCTTGTTGGCACTGGTGTCGTCAGGCATGGAGA 483
                                                                                                                                                                                                                                                                                                          497 TAATACCCTTCCGTATGCTAACCAACTATTATAATTGGCACCATTTTTCACATGCTA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1855 GATGTGGCACCGTATTGATGAAGAGAGAGATAAGAGTTAGAGTTTCATGGAATTAGAGAGGT
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Patent No. US20020046415A1
GENERAL INFORMATION:
APPLICANT: Albert, Henrik H.
APPLICANT: Wei, Hairong
TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Albert, Henrik H.
APPLICANT: Wei, Hairon PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF FILE REFERENCE: UH-03648
CURRENT APPLICATION NUMBER: 08/09/866,153
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 09/270,976
PRIOR APPLICATION NUMBER: 09/270,976
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1451 AGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.9%; Score 118.6; DB 9; Best Local Similarity 86.0%; Pred. No. 7.1e-21; Matches 166; Conservative 0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Saccharum Hybrid Cultivar 32-8560
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CURRENT FILING DATE: 2011-05-24
PRIOR APPLICATION NUMBER: 09/270,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09866153 Patent No. US20020046415A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1629 GCCATGAAATCTC 1641
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Sequence 8, Application US/09866153;
Patent No. US20020046415A1
GENERAL INFORMATION:
APPLICANT: Albert, Henrik H.
APPLICANT: Malbert, Harrong
TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
FILE REPRENCE: UH-03648
CURRENT RILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US/09/866,153
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1914 AGTITICIGAGGCCCGTCTCAGT-GGATTTCATCAGAGTTTCATGGACATTAAATAGGCT 1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1855 GATGTGGCACCGTATTGATGAAGAGAGAGATGATAAGAGTTTCATGGAATTAGAGAGAT 1796
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                                                                                                                                                                                                                                                                                                                                                         3.9%; Score 118.6; DB 9; Length 3691;
llarity 86.0%; Pred. No. 7.1e-21;
Conservative 0; Mismatches 24; Indels 3;
TYPE: DNA
ORGANISM: Saccharum Hybrid Cultivar H32-8560
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)
OTHER INFORMATION: The "n" at position 9 is any nucleotide.
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: (3613)
COTHER INFORMATION: The "n" at position 3613 is any nucleotide.
US-09-866-153-3
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OTHER INFORMATION: The "n" at position 4546 is any nucleotide.
NAME-KEY: misc_feature
LOCATION: (4890)
OTHER INFORMATION: The "n" at position 4890 is any nucleotide.
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Query Match 3.2%;
Best Local Similarity 79.4%;
Matches 127; Conservative
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Matches 105, Conservative
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ORGANISM: Sorghum bicolor
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Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT PRILIGATION NUMBER: US/10/767,701
CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 11451
                                                                                                                                                                                                                                                           1914 AGTTTTCTGAGGCCCGTCTCAGT-GGATTTCATCAGAGTTTCATGGACATTAAATAGGCT 1856
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                                                                                                                                                                                   Gaps
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Pred. No. 2.9e-16;
0; Mismatches 47; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1132 AAACTGCCATTGAGGATGGCCTAAGAGGAGGTTTCTACGAGATTAATG 1085
                                                                                                                                Score 118.6; DB 9; Length 5174;
Pred. No. 8.8e-21;
0; Mismatches 24; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1635 AAATCTCTAGTGACACTGACCTAAGATGAGATTGACTCTAGCACTATG 1682
OTHER INFORMATION: The "n" at position 5125 is any nucleotide.
NAME/KEY: misc feature
LOCATION: (5150)
COTHER INFORMATION: The "n" at position 5150 is any nucleotide.
US-09-866-153-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS3954_1
US-10-767-701-11451
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3.3%;
Best Local Similarity 70.2%;
Matches 160; Conservative
                                                                                                                                    Query Match 3.9%;
Best Local Similarity 86.0%;
Matches 166; Conservative
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US-10-767-701-11451/c
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RESULT 8 US-10-767-701-18110/c

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Sequence 10015, Application US/10767701

Sequence 10015, Application US/2084A1

Sequence 10015, Application No. US20040172684A1

GENERAL INFORMATION:

SEPPLICANT: Exovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REPERENCE: 38-21 (53335) B

CURRENT PAPLICATION NUMBER: US/10/767,701

CURRENT PAPLICATION NUMBER: US/10/767,701

CURRENT PILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQUENCE OF THE PAPER OF THE
Sequence 18110, Application US/10767701

Publication No. US2040172684A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 18110
LENGTH: 398
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Pred. No. 2.1e-15;
0; Mismatches 31; Indels 2;
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US-10-767-701-10015
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; OTHER INFERMATION: Clone ID: LIB3478-007-P1-K1-B12
US-10-767-701-18110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 89.4; DB 18;
Pred. No. 3.8e-13;
0; Mismatches 26;
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80.2%;
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Best Local Similarity 83.3%;
Matches 100; Conservative
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ORGANISM: Zea mays
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US-10-425-114-24208
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cap. Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32756
LENGROUP
                                                                                                        Sequence 42192, Application US/10425115

Sequence 42192, Application US/10425115

Sequence 42192, Application US/2040214272A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Coa, Yought K.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 42192
LENGTH: 2032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 GGCATATTATTAACGAAGAGAGATAAAGGTAAAAAGTTTTATCGAATGAAATGAGTTCCAC 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         618 GGGCGATGAAACTTATGTGCACTGCTTCTAACATATCGGAGTCTTGGGAACATTGACATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1635 AAATCTCTAGTGACACTGACCTAAGATGAGATTGACTCT 1673
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US-10-425-114-32756
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US-10-425-115-42192
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; Sequence 32756, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
  1308 CATCATAAAAC 1318
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ORGANISM: Zea mays
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2.9%; Score 88; DB 17; Length 1894;

Query Match

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Sequence 24208, Application US/10425114

Sequence 24208, Application US/10425114

Publication No. US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: About Xihua

APPLICANT: ApplicANT: Screen, Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 24208

LENGTH: 1285
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Squence 183742, Application US/10425115

Fublication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwile,

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF UNCENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: 2003-04-28

SEQ ID NOS: 369326

SEQ ID NOS: 369326

LENGTH: 1894
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                                                                                           2452 AAAGAGTTAAATGCATGGTAGGCTCTTGATCTTGTCTGGAGGTGCCACTTAGGTCCACAA 2511
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                           Gaps
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Pred. No. 1.2e-12;
0; Mismatches 20; Indels
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2.9%; Score 88; DB 18;
Best Local Similarity 83.3%; Pred. No. 1.2e-12;
Matches 100; Conservative 0; Mismatches 20;
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US-10-425-114-24208
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; OTHER INFORMATION: Clone ID: MRT4577_99156C.1
US-10-425-115-183742
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LENGTH: 1382
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihna
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Wacleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Application Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REPERRICE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 165368
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139 AGACATTGCTGGATGCGCAGCTCCAGCTCTGGCATCACGCTACGTCAAGTCCA 198
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Score 86.2; DB 17; Length 1285; Pred. No. 2.8e-12; 0; Mismatches 23; Indels 0;
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US-10-425-115-142566
  2.9%;
  Query Match
Best Local Similarity 81.33
Matches 100; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                    3014 TGG 3016
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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Plate: 009 row: D column: 09
Seg primer: 17 Promoter Primer.
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tea: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
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Genetica

//mol_type="mkNA"
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/otoe="Jorgan: Lateral buds from field grown adult plants;
/otoe="Jorgan: Lateral buds from field grown adult plants;
/otoe:"Organ: Lateral buds from field grown adult plants;
/otoe: "Jorgan: Lateral buds from field grown adult plants! CDNA was prepared from poly4+ mkNA using SuperScript Plasmid System Kit
(Invitrogen): The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library

.322
 /organism="Saccharum officinarum"

Location/Qualifiers

um cDNA clone SCEZLB1009D09	322 bp mRNA Saccharum officinarum 6454	9D09.g LB1 Sac sequence. 1 GI:34966454	3147 LB100 mRNA 3147	z	RESULT 1 CA113147 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	•
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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SCBGLR1115H12.9 LR1 Saccharum officinarum cDNA clone SCBGLR1115H12
5', mRNA sequence.
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Centro de Biologia Molecular e Engenharia Genetica
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1139
Fax: 55 19 3788 1189
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
thttp://www.bcccenter.fcav.unesp.br
Plate: 115 row: H column: 12
Seq primer: T7 Promoter Primer.
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/large insert library); Vector: pSport1; Site_1: SalI;
                                                                                                                                                                                                                                           TGTGAGAATGTGACAACGGGAGGTCATATCAAGATTCTGG
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0; Mismatches 1; Indels 0
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construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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Matches 321; Conservative
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Site_2: NotI; An unidirectional cDNA library generated from [Leaf roll from field grown adult plants (large linest library)]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 KD were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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Center (BCCC) at
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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Clone distribution: clone distribution
through the Brazilian Clone Collection
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plate: 104 row: B column: 06
Seq primer: T? Promoter Primer.
Location/Qualifiers
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/db_xref="taxon:4547"
/clone="SCSBFL1104B06"
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Saccharum officinarum
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             //note="Organ: Inflorescence at begining of development (Icm-long); Vector: pSport1; Site 1: Sal1; Site_2: Not1; An unidirectional cDNA library generated from [Inflorescence at begining of development (Icm-long)]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 KD were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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SCRFFL1028D06.g FL1 Saccharum officinarum cDNA clone SCRFFL1028D06
                                                                                                                                                                                                                                                                                                                                                                                                     331
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1139
Email: parxuda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at:
Plate: 028 row: D column: 06
Seg primer: T7 Promoter Primer.
                                                                                                                                                                                                                                                                                                                                                                                                272 AGATGAAGAATGTTGATCTGGAGAAGTTTTGTGAAAATGTGACAACAACAGGGAGGTCATA
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                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                         8.4%; Score 254.6; DB 6; Length 556; 97.5%; Pred. No. 5.5e-58; ative 0; Mismatches 4; Indels 3;
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
Contact: All Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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clone lib="FL1"
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CA203163
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/clone libe FEL:
//note="Organ: Inflorescence at begining of development
/note="Organ: Inflorescence at begining of development
(lcm-long); vector: pSporti; Site_1: Sal1; Site_2: NotI;
An unidirectional CDNA library generated from
[Inflorescence at begining of development (lcm-long)].
CDNA was prepared from polyA+ mRNA using SuperScribt
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 KD were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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Saccharum officinarum
Bukaryota, Viridiplanae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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5', mRNA sequence.
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Vettore, A. L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
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Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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Coganism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 164.6; DB 6
Pred. No. 2.7e-33;
0; Mismatches 34
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Contact: Arruda P
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clone="SCRFFL1028D06"
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Seg primer: T7 Promoter Primer
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                            /lab host="DH10B"
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Local Similarity 84.5%;
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50; Indels

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Length 664;

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/clone lib="R22"
/clone lib="R22"
/note="Organ: Shoot-root transition zone from young plants
(small insert library); Vector: pSporti; Site 1: Sall;
Site 2: Not1; An unidirectional cDNA library generated
from [Shoot-root transition zone from young plants (small
insert library)]. CDNA was prepared from poly4+ mRNA
using SuperScript plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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SCSGIR1045G12.g LR1 Saccharum officinarum cDNA clone SCSGIR1045G12
5', mRNA sequence.
CA126310
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1436 TTTGGGGTAGGGTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATG
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Genet. Mol. Bill. 24 (1-4), 1-7 (2001)
Contact: Arruda P.
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Universidade Estadual de Campinas
Gaixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
   organism="Saccharum officinarum"
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Pred. No. 1.7e-31;
0; Mismatches 50;
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Plate: 045 row: G column: 12
Seq primer: T? Promoter Primer.
Location/Qualifiers
                            /mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCVPRZ2042F06"
                                                                                                                                        lab_host="DH10B"
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Spermatophyta; Magnoliophyta; Liliopeida, Poales, Poaceae; PACCAD
clade, Panicoideae; Andropogoneae; Saccharum, Saccharum officinarum
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SCVPRZ2042F06.g RZ2 Saccharum officinarum cDNA clone SCVPRZ2042F06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 042 row: F column: 06
Seg primer: T7 Promoter Primer.
Location/Qualifiers
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Centro de Biología Molecular e Engenharia Genetica
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Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
clone="SCAGLR2018H12"
                                host="DH10B"
                                                                clone lib="LR2"
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CA154373.1 GI:35061389
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CA154373
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/clone="SCBGLR1099C01"
/lab_host="DH108"
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Sorghum bicolor
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Best Local Similarity 93.6
Matches 161; Conservative
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                                                                 /clone lib="LRR"
/clone lib="LRR"
/clone lib="LRR"
/note="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSporti; Site 1: Sall;
Site 2: Not!; An unidirectional cDNA library generated
from [Leaf roll from field grown adult plants (large
insert library]. CDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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SCGIRI1099C01.g LR1 Saccharum officinarum cDNA clone SCBGLR1099C01
5', mRNA sequence.
CA118511
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.uneap.br
Plate: 099 row: C column: 01
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Contact: Arruda P
Contact: Arruda P
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Universidade Estadual de Campinas
Gaixa Postal 6110, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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|db xref="taxon:4547"
|clone="SCSGLR1045G12"
|lab_host="DH10B"
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/note="Crgan: Leaf roll from field grown adult plants
/note="Crgan: Leaf roll from field grown; site_1: Sall;
Site_2: Not1; An unidirectional cDNA library generated
from [Leaf roll from field grown adult plants (large
insert library). cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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1 Dasses 1 to 634)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ACCTTAGGTATCCTGTCTTCCATAGAATTTTCTACCTGAGTAGGTTCGGTCTGGTTGGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CW512557 634 bp DNA linear GSS 07-OCT-20
115_1 10510675_1 30023 Sorghum unfiltered library (LibID: 115)
Sorghum bicolor genomic clone 10510675, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 TCTAGAGCATAGGGATTGTAAAAGCGGTATGCCTCTTCTTCAGTGCAGAATTTCATACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCTAGAGCATAGGCATTGTAAAAGCGGTATGCCTCTTCTTCAGTGCAGAATTTCATACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone lib="Sorghum unfiltered library (LibID: 115)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TTGTAGCGGGTTTCATGCAAATAAGTTAGAAATCGTGCAAACTTGCAATGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorghum genome sequencing by methylation filtration Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contacts Bedell JA,
Contacts Bedell JA,
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 1 row: p column: 17
Seg primer: M13 (40) Forward
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.1%; Score 154.4; DB 6
93.6%; Pred. No. 1.6e-30;
tive 0; Mismatches 11
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/mol_type="genomic DNA"
/cultivar="ATx623"
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Location/Qualifiers
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clone="10510675"
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/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, enter-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into B. coli cells. This is a standard (unfiltered) whole genome shotgun library."
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/lab host="DH108"
/clone_lib="ST3"
/clone_lib="ST3"
/note="Organ: Fourth apical stalk internodes of adult plants; Vector: pSport1; Site_1: Sal1; Site_2: Not1; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using SuperScribt Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated
                                                                                                                                                                                                                                                                                                                        1425 ATGACTTATCATTTGGGGTAGGGAGTAGGTTTCTAAGGCCAGTCTCAGTGGGGTTTCATC 1484
                                                                                                                                                                                                                                                                                                                                                                                                                          1545 AAGAGTTTCATGCGAGTAGAGAGTTTCATGGGGATGAAACTCTTCTTCACTGTTTCCA 1604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bmail: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 117 row: A column: 08
Seg primer: SP6 Promoter primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 ACATATTGATGTTGGAAACTGTGTGAAACTCCCATTGAGGATGACCTAAGGT 258
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                         ٠,
                                                                                                                                                                                                                     Length 634;
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Contact: Arruda P Centro de Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas
Caixa Poetal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137
Fax: 55 19 3788 1109
                                                                                                                                                                                                                                                                    0; Mismatches 53; Indels
                                                                                                                                                                                                                  Score 152.2; DB 9;
Pred. No. 6.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA186194
CA186194.1 GI:35125729
                                                                                                                                                                                                          5.0%;
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Saccharum officinarum
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                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                 Matches 184;
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VERSION
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AUTHORS
TITLE
JOURNAL
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CL192172 114_32247_052 Sorghum methylation-filtered library (LibID: 104) Sorghum bicolor genomic clone 10940055, genomic survey
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Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Surghum bicolor
Surghum bicolor
Surghum
Surghum
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 71)
Budiman,Ma., Flick,T., Jones,J., Nunberg,A., Citek,R.W.,
Robbins,D., Rohlfing,T., Bradford,K., Fries,J., McMenamy,J.,
Trani,L., Isak,A., Zimmerman,C., Lakey,N. and Bedell,J.A.
GeneThresher methylation filtered genomic sequences from Sorghum
                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                          398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 TACTGGCTGAGATGCCATTGTTGTGTAGATCGAGAGAAACGAGAAGAATGCTAGTCTAAT 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Sorghum methylation-filtered library (LibID: 104)"
in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into t vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                         279 GAATGTTGATCTGGAGAAGTTTTGTGAGAATGTGACAACAACGGGAGGTCATATCAAGAT
                                                                                                                                                                                                                                                      302 GGATGTTGATCTTAGAGAAGTTCTGTGAGGATGTGACAATAACAGGAGGTCGTATCAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 AATTGGCTGAGATGCAATT-TTGTGTAGATAAAGAGAAACGAGAAGAATGCTAAT
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                                                                                                                                                                                 22;
                                                                                                                                           Length 400;
                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2004)
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
71: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
                                                                                                                                           Score 149.2; DB 6;
Pred. No. 3.9e-29;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
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Location/Qualifiers
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Seg primer: M13/pUC Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:40704695
                                                                                                                                         tch 4.9%;
al Similarity 83.5%;
202; Conservative
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CL192172.1
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharum officinarum
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae; PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into Hincil-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation-filtered library."
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/note="Organ: Developed inflorescence and rachis (20cm-long); Vector: pSport1; Site_1: Sall; Site_2: Not1; (20cm-long); Vector: pSport1; Site_1: Sall; Site_2: Not1; An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing
                                                                                                                                                                                                                                                                                                                                                     182
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                                                                                                                                                                                                                                                                                                                                243 ATCCCCATGAACTCCTATGCACTGTTTCCAAAATATTGATGTGTTGGAAACTGTGTCTT
                                                                                                                                                                                                                                                                                                     1454 TTTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGAT
                                                                                                                                                                                                                                                  Gaps
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Universidade Estadual de Campinas
Universidade Estadual de Campinas
Universidade Estadual de Campinas
Tedis 59 93 98 1137
Fax: 55 19 3788 1137
Fax: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parvuda@unicamp.br
Clone distribution: clone distribution information can be ithrough the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 023 row: E column: 04
Seq primer: T7 Promoter Primer.
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                                                                                                                                                                                            4.9%; Score 148.6; DB 9; Length 717; 79.9%; Pred. No. 6.7e-29; tive 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAATCTCTAGTGACACTGACCTAAGATGAGATTGACTC 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAACTCCCGTTGAGGATGGCCTAAGAGTAGAGAGTTTC 341
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/organism="Saccharum officinarum"
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/db_xref="taxon:4547"
/clone="SCRUFL4023E04"
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                                                                                                                                                                                                                         Best Local Similarity 19.9
Matches 175; Conservative
                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                    545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   605
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between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorghum bicolor

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 740)

Budiman, M.A., Filck, B., Jones, J., Nunberg, A., Citek, R.W.,

Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McMenamy, J.,

Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A.

GeneThresher methylation filtered genomic sequences from Sorghum
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                                                                                                                                                                                                                                                                                                                                                                 486 TACCATATTAATGAAGAGAGAGATGATAAGAGTTTCATGGAAGTAGAGGAGAGTTTCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             546 GGATGAAACTCTTCTGCACTGTTTCCAAAATCTGGATGTTGGAAACAGTGACATGAAA
                                                                                                                                                                                                                                            1458 TAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATGTGA
                                                                                                                                                                                                                                                                                      427 TAAGGCCAGTCTCAAT-GAGTTTCATCAGAGTTTCATAGACATTAATTATGCTGATGTGG
                                                                                                                                                                                                                                                                                                                                     1578 GGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTGGTAAGAGGGCCATGAAA
                                                                                                                                                                                               Gaps
                                                                                                                                                                                               1;
                                                                                                                                                  Length 669;
                                                                                                                                                                                            27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Badell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USP
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 414 row: f column: 03
Seq primer: M13/pUC Forward
Class: Shotgun
High quality sequence stop: 740.
                                                                                                                                           Score 147.8; DB 6;
Pred. No. 1.1e-28;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .740
/organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4558"
/clone="10939851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1638 TCTCTAGTGACACTGACCTAAGA 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           606 TTCCCACTGAGACTGGCCTAATA 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor (sorghum)
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                                                                                                                                           4.9%;
                                                                                                                                             Query Match
Best Local Similarity 86.2
Matches 175; Conservative
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CL191874
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ic83e09.gl WGS-SbicolorF (JM107 adapted methyl filtered) Sorghum bicolor genomic clone ic83e09 5', genomic survey sequence. BZ342445
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//lab_host="J70107 or DH5a"
//clone liba-wGS-SbicclorF (JM107 adapted methyl filtered)"
//clone liba-wGS-SbicclorF Xba I; The vector was
digested wich Xba I; Site_2: Xba I; The vector was
digested wich Xba and one nucleotide was added by fill in
the recessive 3, end. The genomic DNA was nebulized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (:x/y reads in Mi3mpl9,
elther JM107 or DH5a."
                                                                                                                                                                                            188
                                                                                                                                                                                                                                                                                      248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Wagnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Sorghum.

(Dases 1 to 787)

Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N., Zutzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Genomic shotgun sequences from Sorghum bicolor (methyl-filtered) Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                             249 TAGGGATGAAACTCCTIGTACATTGTTTTTAAAATATGGATGTGGAAACTGAGCCATG, 308
                                                                                                                                                                                                                                                                                   189 TGGCACCGTATTAATGAAATAGAGGTGATAAGAGTTTCATGAGAGTAGTGGAGATTTTA
                                                                                                                                              1455 TTCTAAGGCCAGTCTCAGTGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATG
                                                                                                                                                                                          130 TACTAAGGCCAGTCTCAAT-GGGTTTCATTAGAGTTTCATGGATATTAAATATGCTGATG
                                                                                                                                                                                                                                        1515 TGACACCGTATTGATGAAGAGAGATGATAAGAGTTTCATGCGAGTAGAGAGTTTCA
                                                                                                                                                                                                                                                                                                                                 TGGGGATGAAACTCTTCTTCACTGTTTCCAAAATATAGATGCATTGGTAAGAGGGCCATG
                                                                                                     Gaps
                                                                                                   1;
                                                     Length 1273;
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                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 515 367 8884
Exa: 516 367 8874
Email: mccombie@cshl.org
                                                  Score 141.8; DB 8;
Pred. No. 5.8e-27;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                           1635 AAATCTCTAGTGACACTGACCTAAGATGAGATT 1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 139.4; DB 8 Pred. No. 2.3e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341
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High quality sequence stop: 787.
Location/Qualifiers
1. 787
/organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 AAACCTACACTGAGAATGATCTAAGAGTCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="ic83e09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: ic83 row: e column: 09
Seg primer: -21M13UnivRev
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Sorghum bicolor
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                                                4.7%;
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                                                Query Match
Best Local Similarity 82.2
Matches 175; Conservative
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Best Local Similarity
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BZ342445
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SP_Ba0033E12 3', genomic survey sequence.
                                                                                                4
                                                                                                                                    1340 ACATTTAGTTGGTATCATAAATATTATTAT--TATCATAAAATTTGATCAACTTGAG 1397
                                                                                                                                                                                                                                ATGCTTTGACTCTTCAAGATTCTTGGAATGACTTATCATTTGGGGGTAGGGAGTAGGTTTC 1457
                                                                                                                                                                                                                                                                                                                          TAAGGCCAGTCTCAGGGGTTTCATCAGAGTTTCATGGACATTAAATAAGCTGATGTGA 1517
                                                                                                                                                                                                                                                                                                                                                                                                                   1578 GGATGAAACTCTTCACTGTTTCCAAAA--TATAGATGCATTGGTAAGAGGGCCCATGA 1635
                                                                                                                                                                 340 TTAGGCCAGTCTCAATGGGATTTCATTAGAGTTTCATGCACATTAAAATATGC--ATATGA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukäryotä, Virädiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 1273) Andropogoneae; Sorghum.

1 (bases 1 to 1273) Andropogoneae; Sorghum.

Soderlund, C. and Hatfield, J. Sollura, K., Pries, G., Currie, J., Sequencing of Sorghum BAC ends.

Thtp://genome.arizona.edu/stc/sorghum

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 CACTGTATTTATGA--AGAGAGATGATAAGAATTTCATAAAAGTAGAAATAATTTTATCC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 CTATAAAACTCTTTTGCGCTATTTTAAAATCTAAATATGTGTTAGAACTAGATCATCATCA 515
                                                                                                Gaps
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Corganism="Sorghum propinguum"
/mol types = "sorghum propinguum"
/mol types = "sorghum propinguum"
/db_xref="teaxon:132711"
/clone="sp_ Ba0033B12"
/clone="sp_ Ba003B12"
/note=="yector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
ST1-0088, USA
Tel: 520 626 348
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                           8
                                                Length 740;
                                                                                           76; Indels
                                                  DB 9;
                                             Score 147.4; DB 9
Pred. No. 1.4e-28;
0; Mismatches 76
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Class: BAC ends.
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BACKWARD: gta aaa cga cgg cca gtg
Plate: 0033 row: E column: 12
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                                      4.9%;
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                                                                                         Matches 241; Conservative
                                                                      Similarity
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                                             Query Match
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                                                                      Best Local
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1; Gaps

0; Mismatches 36; Indels

Matches 172; Conservative

Search completed: February 16, 2005, 10:23:23 Job time : 9459 secs

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